

BioXM™ Knowledge Management Environment

Quick Start

BioXM version 5.0 (252)
January 2014

Biomax Informatics AG



BioXM™ Knowledge Management Environment: Quick Start

Biomax Informatics AG

BioXM version 5.0 (252)

Publication date January 2014

Copyright © 2014 Biomax Informatics AG

Biomax Informatics AG; Sitz: Martinsried bei München, Amtsgericht München, HRB 134442; Ust-IdNr. DE 191 603 142; Steuer-Nr.: 143 / 100 / 10945; Vorstand: Dr. Klaus Heumann; Vorsitzender des Aufsichtsrates: Prof. Dr. Hans-Werner Mewes

Biomax and BioXM are registered trademarks of Biomax Informatics AG in Germany and other countries. Registered names, trademarks, etc., used in this document, even when not specifically marked as such, are not to be considered unprotected by law.

Table of Contents

Quick Start	1
1. Designing the data model	1
1.1. Starting the BioXM system	1
1.2. Displaying the data model	2
1.3. Adding element types	2
1.4. Adding a relation class	3
1.5. Adding an annotation form	4
1.6. Mapping BioRS entries	6
1.7. Associating an ontology	10
1.8. Defining object type scopes	11
1.9. Defining relation class scopes	14
1.10. Saving the data model layout	15
1.11. Displaying a saved data model layout	15
2. Importing data	17
2.1. Defining the import	17
2.2. Configuring the tab import script	19
2.3. Simulating the import	24
2.4. Trouble-shooting the import	25
2.5. Completing the import	26
3. Preparing views and queries	28
3.1. Creating a view	28
3.2. Displaying the view	35
3.3. Creating a query	36
3.4. Displaying the query results	37
3.5. Redefining the query	39
3.6. Saving the query and creating a smart folder	40
3.7. Editing the smart folder	40
4. Preparing a BioXM web portal	43
4.1. Logging into a BioXM web portal	43
4.2. Setting up a query in the BioXM web portal	44
4.3. Displaying an object report in the web portal	49
5. Getting help	54
6. Logging out	54
6.1. Logging out of the BioXM client application	54
6.2. Logging out of the BioXM web portal	54

Quick Start

The BioXM™ Knowledge Management Environment is a project-centered, distributed platform that facilitates communication and collaboration in a research environment. The BioXM system provides a central inventory of information describing a particular area of research, making it easy for users to stay in touch with recent additions or changes in knowledge that should be available to the entire organization. In addition, the BioXM system provides a personalized work environment which supports user and project groups. This environment allows researchers to focus specifically on generating knowledge in a particular scientific field.

This document describes the basic steps from getting started with an empty instance of the BioXM Knowledge Management Environment to creating a productive "gene index" knowledge base:

1. Designing the data model
2. Importing data
3. Preparing views and queries
4. Preparing a BioXM web portal

These steps will allow a personalized work environment to be created using tailored views, smart folders and a BioXM web portal.



Tip

For more information about the BioXM Knowledge Management Environment, see the *BioXM User Manual*. Before using the BioXM system for the first time, you may want to read the overview of the basic BioXM concepts and tools in the *BioXM User Manual*.

1. Designing the data model

The first step in building a knowledge base is to design the domain-specific data model in the BioXM Knowledge Management Environment. In the example use case shown here, we will create a "gene index" knowledge base using the following seed data: a table of gene names, synonyms, EntrezGene identifiers (IDs) and Gene Ontology (GO) classification. A sketch of how we want to structure the data model is shown below.

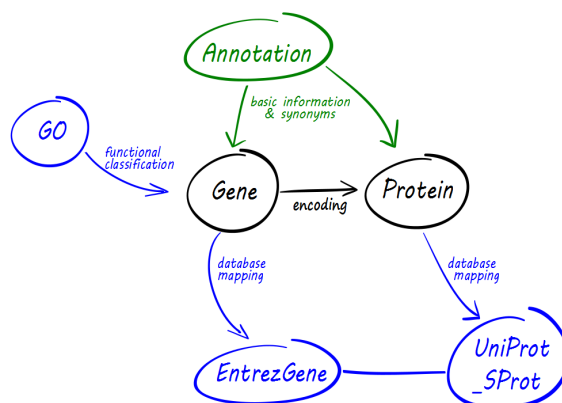


Figure 1. Sketch of a data model

1.1. Starting the BioXM system

To start the BioXM client, complete the following steps.

1. Start the BioXM client (e.g., by entering the uniform resource locator (URL) of your BioXM instance in a browser). The login page will be displayed.
2. Enter your user name and password and click the **"Login"** button.

The BioXM Knowledge Management Environment application will start and the main application window will be displayed.

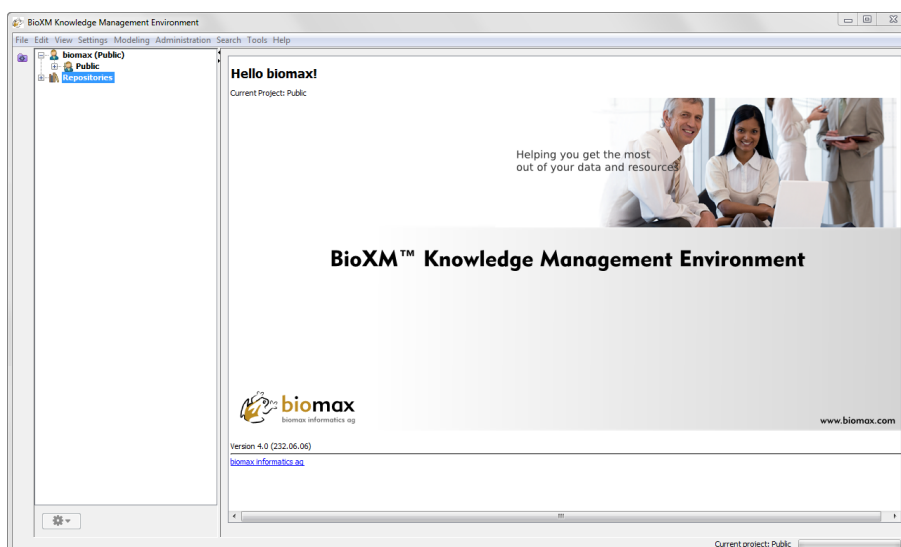


Figure 2. BioXM main application window

1.2. Displaying the data model

The BioXM system provides a graph viewer for visualization of semantic objects and the connections between them as well as exploration of the resulting semantic network (or data model). The BioXM graph viewer renders the data model as an interactive white board so semantic objects and associated objects in a data model can be easily added, deleted, edited and visualized. The graph viewer allows this editing and extension while enforcing consistency within the data model. To display the data model graph, complete the following steps.

1. Select "*Modeling → Visualize data model*" in the main menu to display the "Visualize data model" dialog.
2. Select "New visualization" and click the "**OK**" button to display the data model graph.

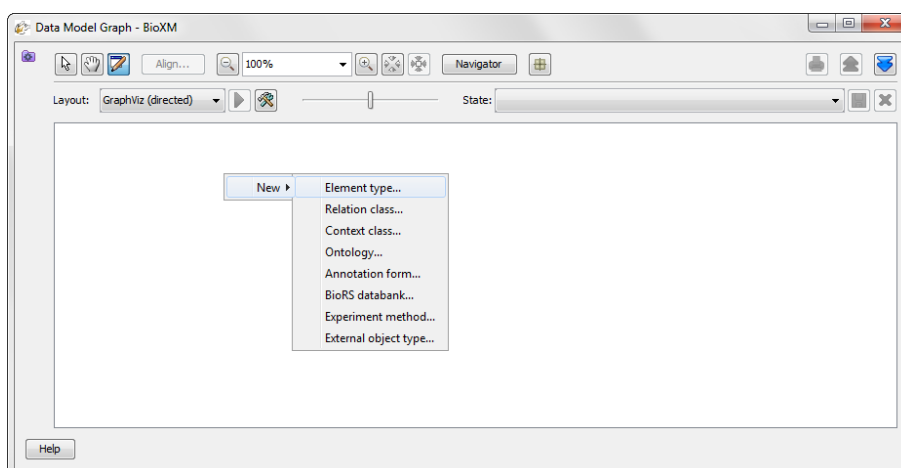


Figure 3. Data model graph with open context-sensitive menu

1.3. Adding element types

The data model will have two types of elements: genes and proteins. The properties of the elements are defined by the element type. Before adding the data, relationships and annotation for the elements, we will add the element types to the data model.

1. Right-click anywhere in the empty field of the data model graph to display a context-sensitive menu. Select "*New → Element type*". The "New element type" dialog will be displayed.

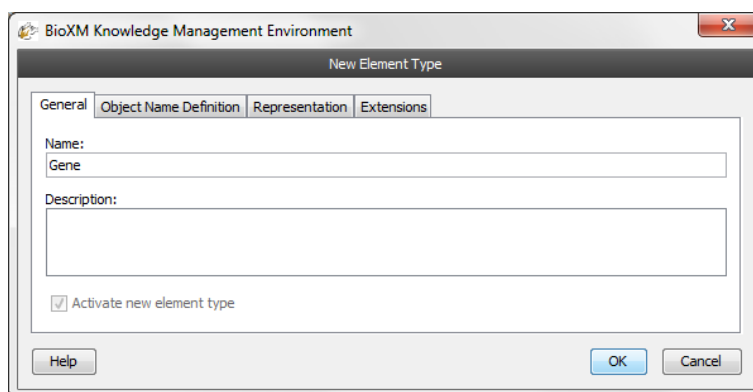


Figure 4. Adding a new element type

2. Enter the name, e.g., "Gene" in the field.

We will use the default settings for the other tabs: "Object Name Definition" (used to set the element name to be controlled by a certain pattern), "Representation" (used to define how the element appears in the interface) and "Extensions" (used to set extensions for the element type). Click **"OK"**.

The "Gene" element type will appear in the data model graph.

3. Complete the steps again to add a protein element type. Instead of "Gene" enter "Protein" in the "Name" field. The "Protein" element type will appear in the data model graph.

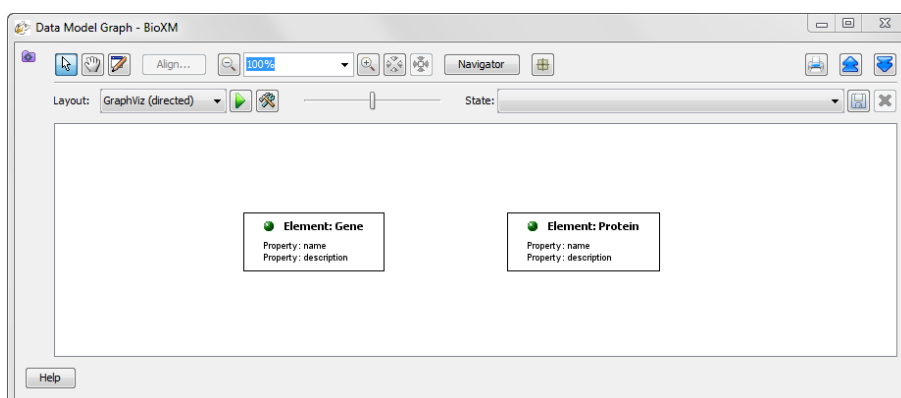



Figure 5. Data model graph with elements

1.4. Adding a relation class

To create the relationship between genes and proteins in the data model, we will add a relation class to define the relationship between the gene element type and protein element type.

1. Using the select tool  (in the upper left corner) add a relation class by dragging-and-dropping one element onto another. For our use case, drag the "Gene" element type to the "Protein" element type.
2. Select *"Create relation class: from 'Element: Gene' to 'Element: Protein'"* from the menu. The "New relation class" dialog will appear.

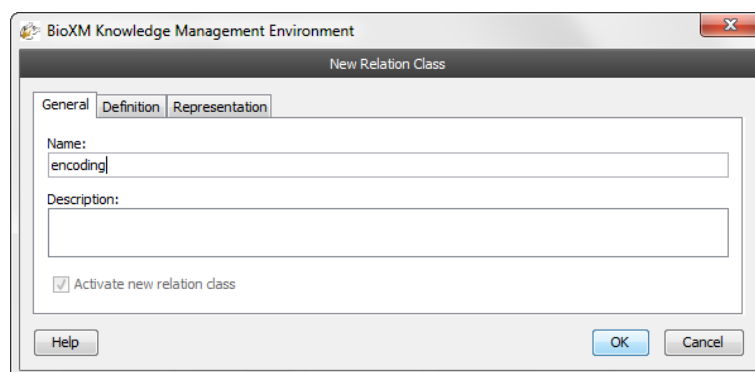


Figure 6. Adding a new relation class

3. In the "General" tab, enter "encoding" in the name field. In the "Definition" tab, enter "encodes" in the "Forward Name:" field and "is encoded by" in the "Backward Name:" field. We will use the default settings in the "Representation" tab. Click the "OK" button.

The "Relation: encoding" will appear in the data model graph.

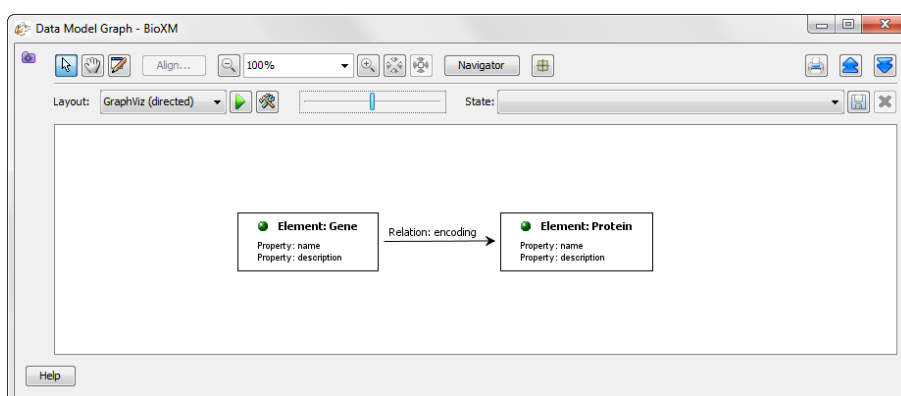


Figure 7. New relation class in the data model

1.5. Adding an annotation form

To add some basic information (including synonyms) to the genes and proteins, we will add a new annotation form called "Basic information" to the data model and associate it with the gene and protein elements.

1. Right click on the whitespace in the data model graph to display the context-sensitive menu. Select "New... → Annotation form..." from the drop-down menu. The "Create new annotation form" dialog will be displayed.

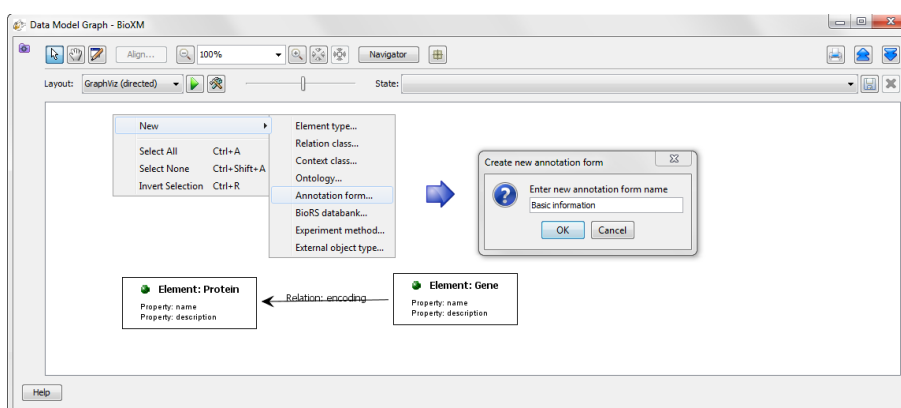


Figure 8. Adding a new annotation form to the data model

2. Enter a name (e.g., "Basic information") for the new annotation form in the field and click **"OK"**. The "Annotation: Basic information" form will be displayed in the data model graph.

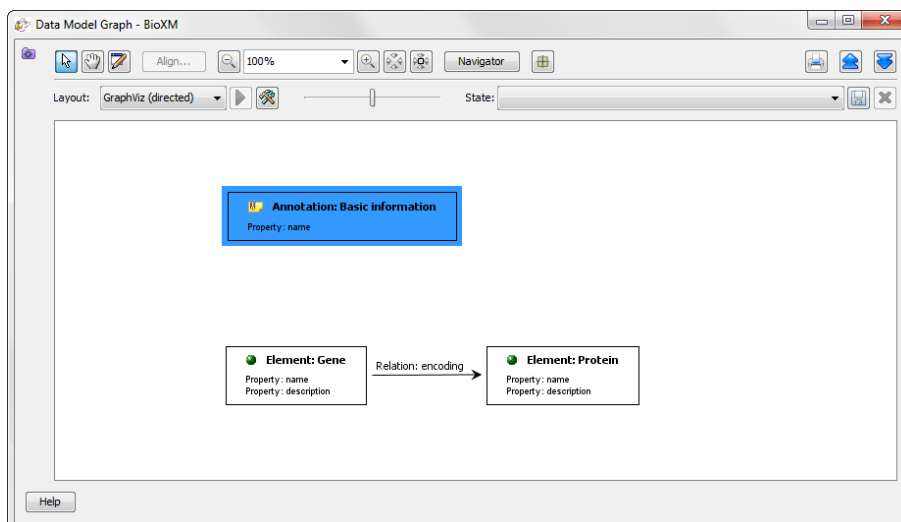


Figure 9. New annotation form in the data model

3. Right click the "Annotation: Basic information" form and select *"Edit"* from the menu to display the "Edit annotation form" dialog.

The screenshot shows the 'BioXM Knowledge Management Environment' window. The dialog is titled 'Edit annotation form: Basic information'. It has two main sections: 'Properties' and 'Attributes'. The 'Properties' section has a 'Name' field with the value 'Basic information' and a 'Description' field. The 'Attributes' section has a large empty text area. Below the text area, it says 'No attribute is selected' and has three buttons: 'Add...', 'Edit...', and 'Remove'. There is also a checkbox labeled 'Use example value as default'. At the bottom of the dialog are 'Help', 'OK', and 'Cancel' buttons.

Figure 10. Editing an annotation form

4. In the "Attributes" section, click the **"Add..."** button to display the "Edit annotation form" dialog.

Figure 11. Adding an attribute to an annotation form


Enter a name for the attribute ("Synonyms") and a description (optional) in the text fields. Set the type to be "Text". Click the **"Next"** button.

- Under "Attribute value properties" check the "Multiple values allowed" option. Click the **"Finish"** and the **"OK"** buttons to return to the data model graph.



Tip

Under "Attribute type properties" you can also select the "Controlled by pattern" option and set a pattern (i.e., a regular expression) to control the input data.

- Using the select tool  assign the annotation form to the gene element by dragging and dropping it onto the gene element type. Likewise, drag and drop the annotation form onto the protein element type.

The annotation form is now assigned to the gene element type and the protein element type.

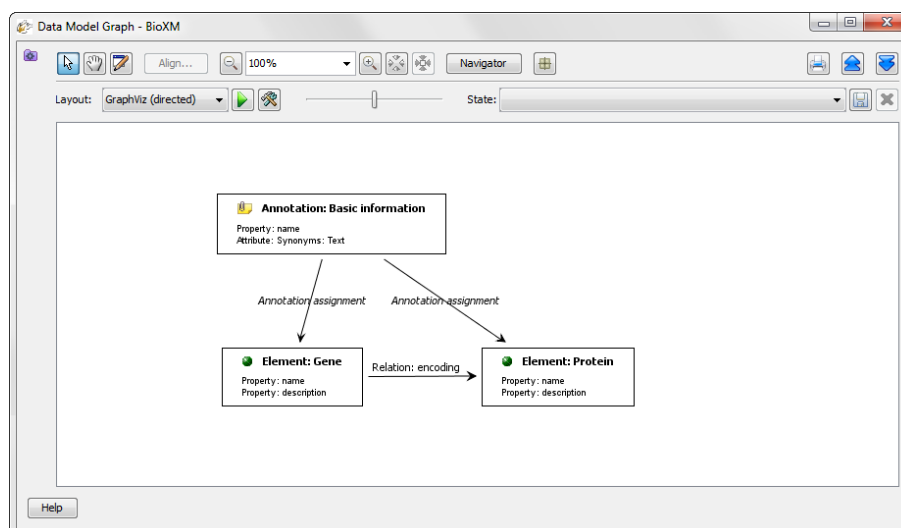


Figure 12. Assigning an annotation form

1.6. Mapping BioRS entries

Next we will map the "Gene" and "Protein" elements to external database entries integrated using the BioRS system (BioRS databanks). Genes will be mapped to the EntrezGene databank and proteins will be mapped to the UniProt Swiss-Prot databank.

1. Right click on the whitespace in the data model graph to display the context-sensitive menu. Select "New → BioRS databank...". The "New BioRS Databank" dialog will be displayed.

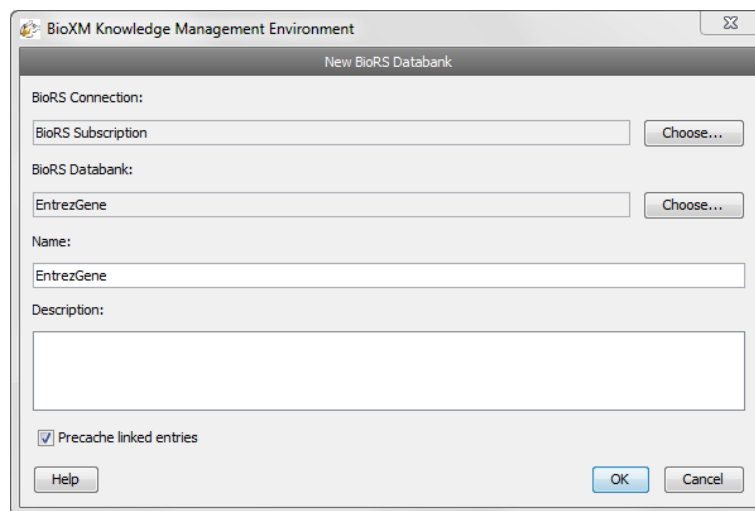



Figure 13. Adding a new BioRS databank

2. Click the "**Choose**" button to display the BioRS connection options, select a BioRS connection by clicking it in the list and click "**OK**".
3. Likewise, click the "**Choose**" button to display the available BioRS databanks, select a databank and click "**OK**". For this use case, select the "EntrezGene" databank.
4. Click the "**OK**" button in the "New BioRS Databank" dialog. The "EntrezGene" databank will appear in the data model graph.
5. Using the select tool  assign the gene element type to the databank by dragging-and-dropping the "BioRS entry: EntrezGene" to the "Element: Gene" and selecting the "Assign 'Element: Gene' to BioRS databank 'EntrezGene'" option from the context-sensitive menu.

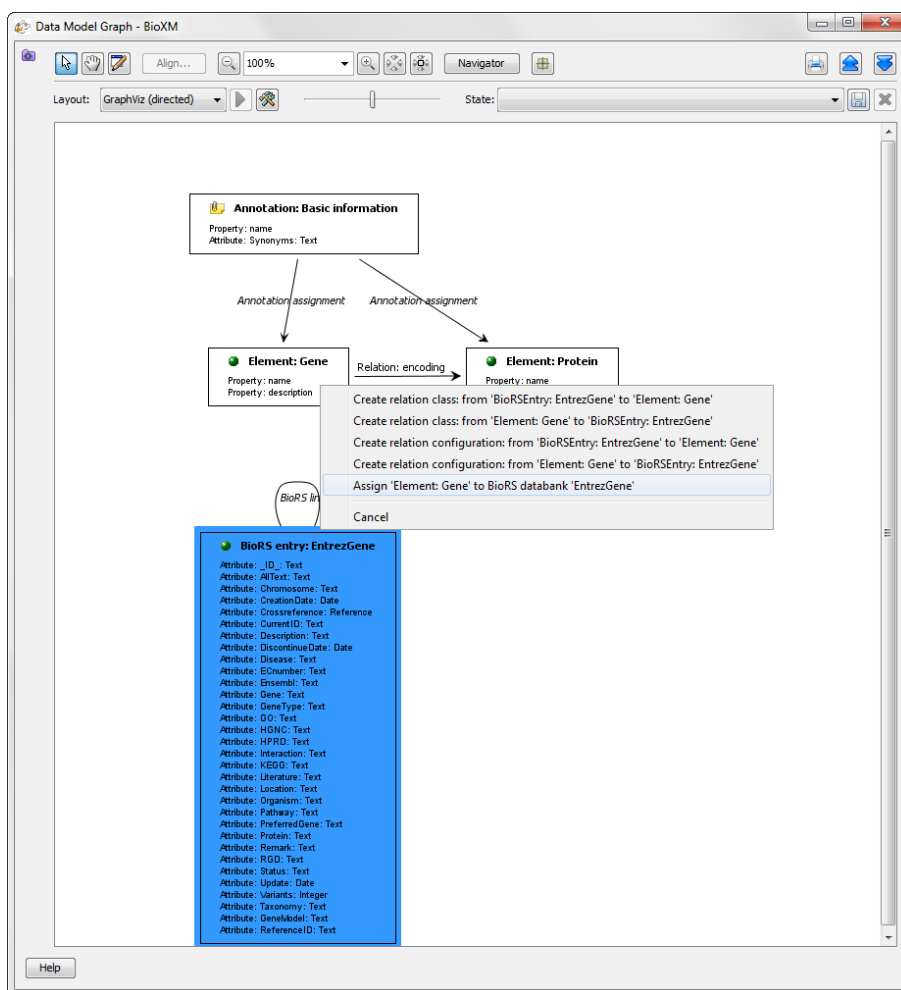


Figure 14. Assigning an element to a BioRS databank

An assignment is created between the two. Assignments differ from relations as follows:

- Assignments are preferred if using a data set as the basis of an object definition; extra information cannot be added. Assignments are indicated by italic text in the data model graph.
- Relations are semantic relationships; extra information can be added using annotation forms.

To add the UNIPROT_SPROT databank and assign the protein element type to it, complete the steps again. In Step 3, select the "UNIPROT_SPROT" BioRS databank. In Step 5, drag the "BioRS entry: UNIPROT_SPROT" to the "Element: Protein".

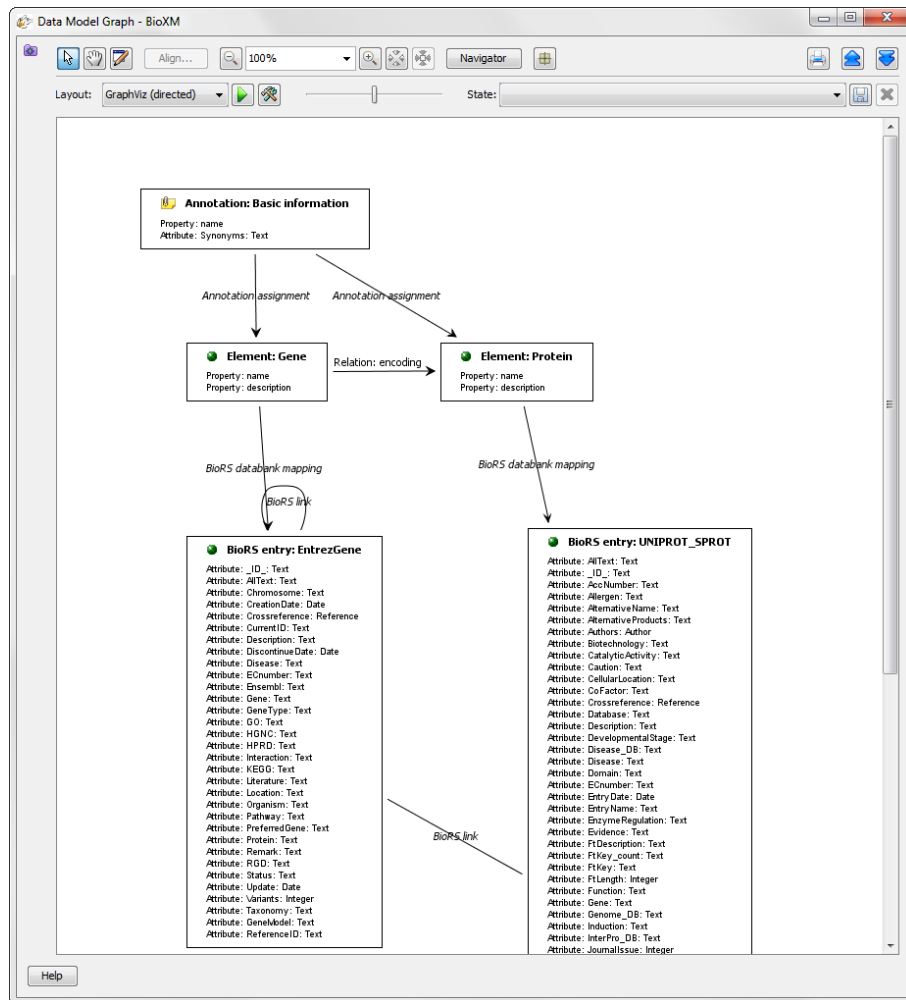


Figure 15. BioRS databanks in the data model

The BioRS databanks have been added to the data model. Additionally, the BioRS databanks are available in the "BioRS entries" repository in the project tree of the BioXM client. In fact, all object types configured in the data model graph are available under "Repositories" in the project tree. As the objects are configured and their scopes are defined, the repositories corresponding to the object types become available automatically. Note that the graphic below shows the project tree for the finished data model. In the current step only the "BioRS entries" and "Ontologies" repositories are shown. Other repositories will be added after defining the scopes.

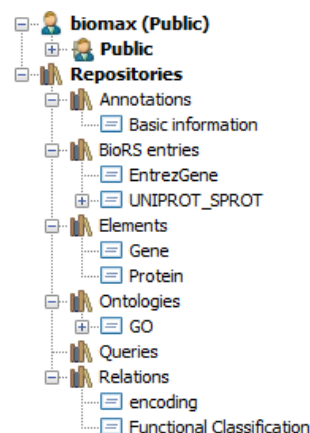


Figure 16. Object types of the data model in the project tree

1.7. Associating an ontology

Next we will add an ontology to the data model. Ontologies, a central concept in knowledge management, relate the conceptualization of a domain to the data model. Ontologies are often developed by domain experts as a set of “scientific nomenclature” and are widely used in the sciences. We will associate the GO ontology with the “Gene” elements.

The GO ontology has already been imported into the BioXM system and is available in the project tree in the “Ontologies” repository of the project tree (see Figure 16: “Object types of the data model in the project tree”). We only need to associate the ontology with the “Gene” elements. (For more information about importing an ontology, see the *BioXM User Manual*.)

1. If the “Ontology entry: GO” is not already displayed in the data model graph, it needs to be displayed. From the main menu, select “Modeling → Visualize Data Model” to display the “Visualize Data Model” dialog.

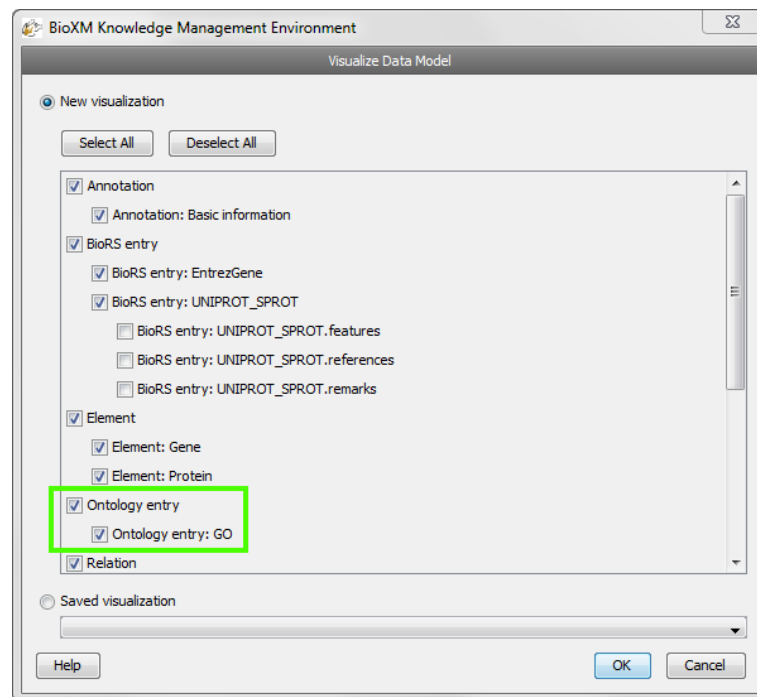


Figure 17. Setting what is displayed in the data model graph

2. Click the “**Select all**” button or check the “Ontology entry: GO” check box. Click the “**OK**” button. The “Ontology entry: GO” will be displayed in the data model graph.

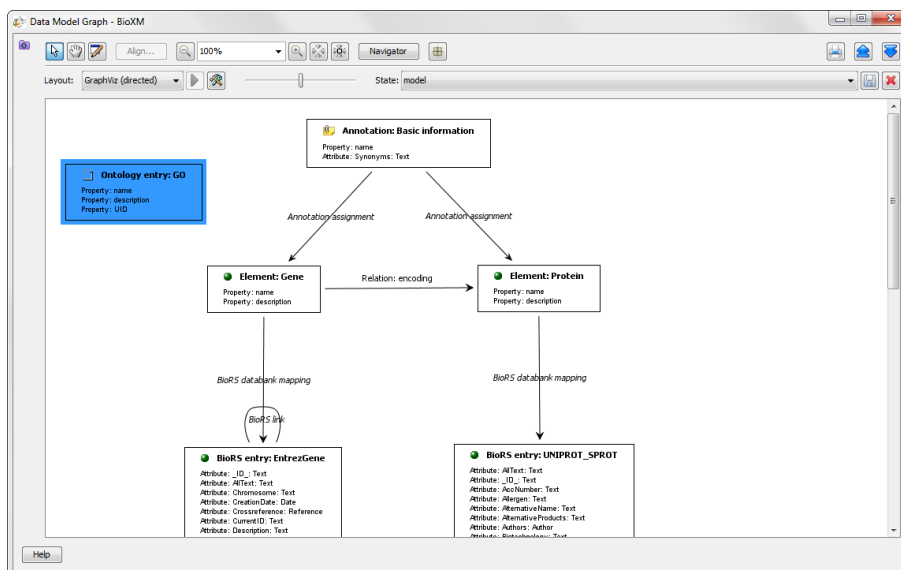


Figure 18. Displaying the GO ontology in the data model graph


- Using the select tool  drag the "Ontology entry: GO" to the "Element: Gene". Select "Create relation class: from 'Ontology Entry:GO' to 'Element:Gene'" from the context-sensitive menu. The "New Relation Class" dialog will be displayed.

Figure 19. Defining a new relation class

- In the "General" tab, enter a name for the relation class (e.g., "Functional Classification"). In the "Definition" tab, enter a forward name (e.g., "classifies") and a backward name (e.g., "is classified by") in the fields. Click "OK" to close the dialog.

The GO ontology will be related to the "Gene" element type.

1.8. Defining object type scopes

Next we will define the scopes for the object types. Scopes allow semantic objects of a specific class or type to be restricted to a defined set of projects, i.e., the object type scope defines the project(s) in which the object type can be used. The "Global Scope" setting allows the object type scope to be set to all projects. Objects based on object types with the "Global Scope" setting can be created within any project, including any new projects that may be created.

Special assignments (e.g., annotation assignments, BioRS databanks and ontologies) are not scope-capable, but are considered to have the "Global Scope" setting. That is, they can be used in all projects. Elements (such as Gene and Protein), relations and annotations, on the other hand, are scope-capable and can be restricted to certain projects. In this use case, however, they will be given the "Global Scope" setting.

- In the data model graph, right click an element (e.g., "Element: Gene") and select "Scopes..." from the context-sensitive menu.

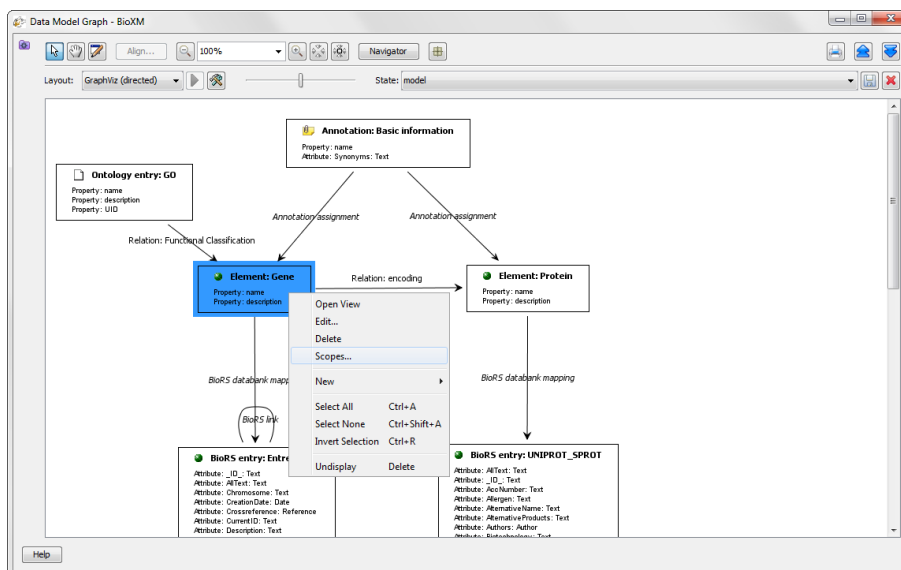


Figure 20. Opening the "Object Type Scopes" dialog for an element type

Alternatively, select "*Modeling* → *Element types...*" in the main menu to display the "Element types" dialog.

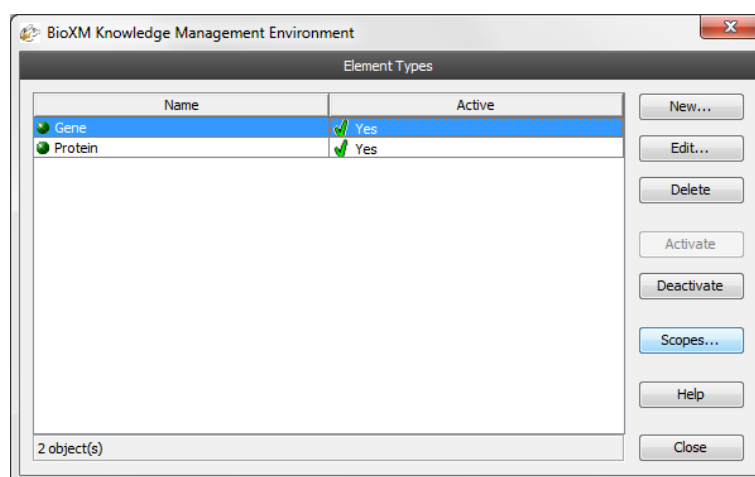


Figure 21. Opening the "Object Type Scopes" dialog via the "Element types" dialog

2. Select a element type and click the "**Scopes...**" button to display the "Object Type Scopes" dialog.

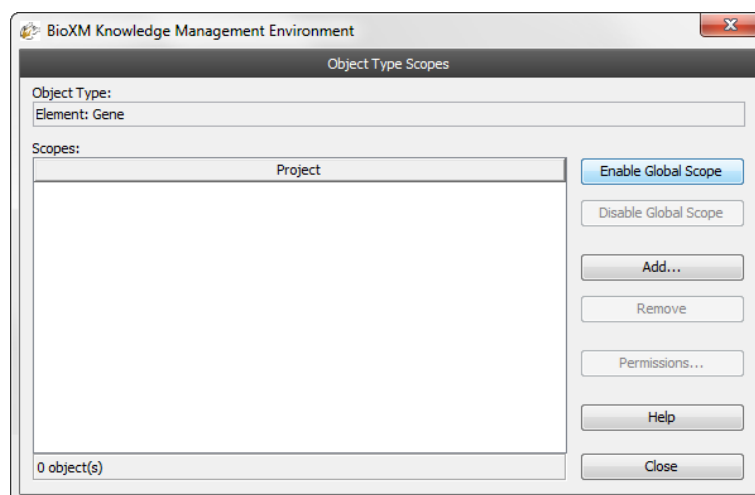



Figure 22. Setting an element type scope

3. Click the **"Enable Global Scope"** button. After the scope is set, click **"Close"** to close the dialog window.

Alternatively, a new scope could be defined to restrict the element's use to certain projects by clicking the **"Add..."** button in the "Object Type Scopes" dialog and selecting the desired projects in the "New Scopes" dialog. In this use case, however, all scope-capable items should be given the "Global Scope" setting.

4. Complete the steps again to set the rest of the scope-capable items (i.e., "Element:Protein" and "Annotation: Basic information") to have the "Global Scope".
5. The scope settings can be displayed in the data model graph by clicking the **"Toggle scope display"** button  (at the top of the window). The projects in the scope are displayed for each scope-capable item in the data model (e.g., "Project: Public").

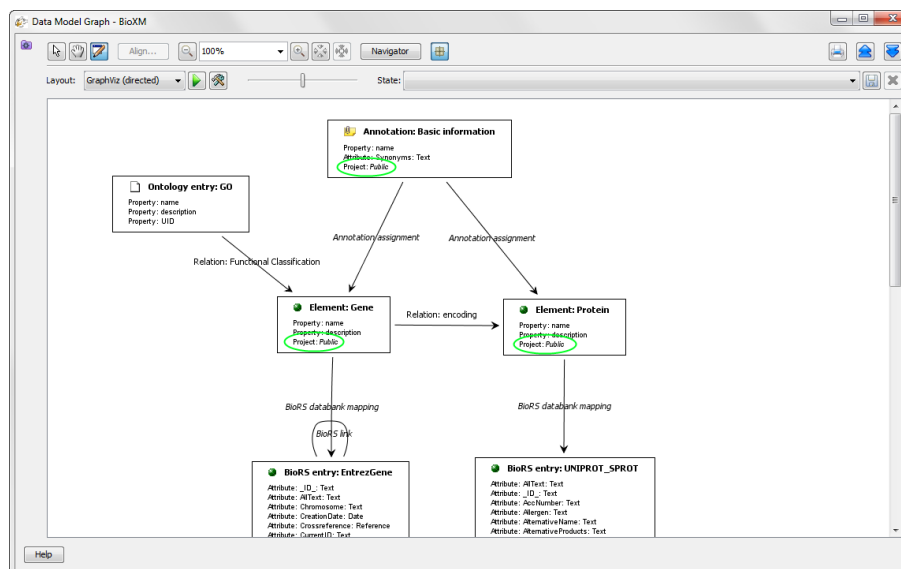


Figure 23. Displaying scopes in the data model graph

Upon defining the scopes, the elements and annotation become available in the "Repositories" folder of the project tree (see Figure 16: "Object types of the data model in the project tree"). The "Gene" and "Protein" element types are found in the "Elements" repository. The "Basic information" annotation form is found in the "Annotation" repository.

1.9. Defining relation class scopes

Next we will define the scopes for the relation classes. Like scopes for objects, relation class scopes define the project(s) in which a relation class can be used. Relation classes set to the "Global Scope" setting can be created within any project, including any new projects that may be created.

1. In the data model graph, right click a relation (e.g., "Relation: Functional Classification") and select "Scopes..." from the context-sensitive menu.

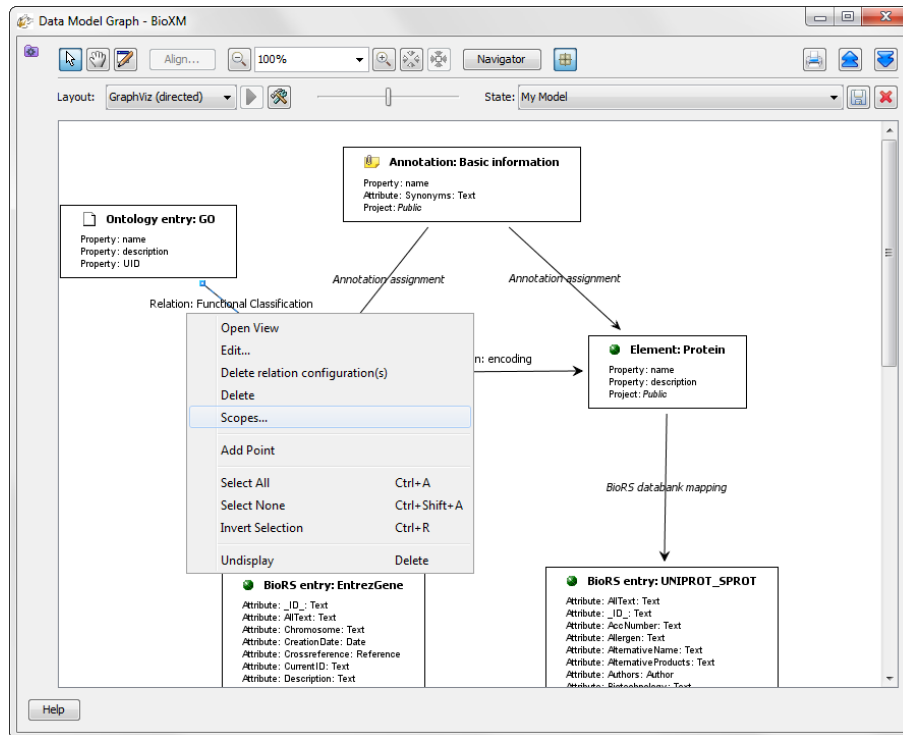


Figure 24. Opening the "Object Type Scopes" dialog for a relation class

Alternatively, select "Modeling → Relation classes..." in the main menu to display the "Relation classes" dialog.

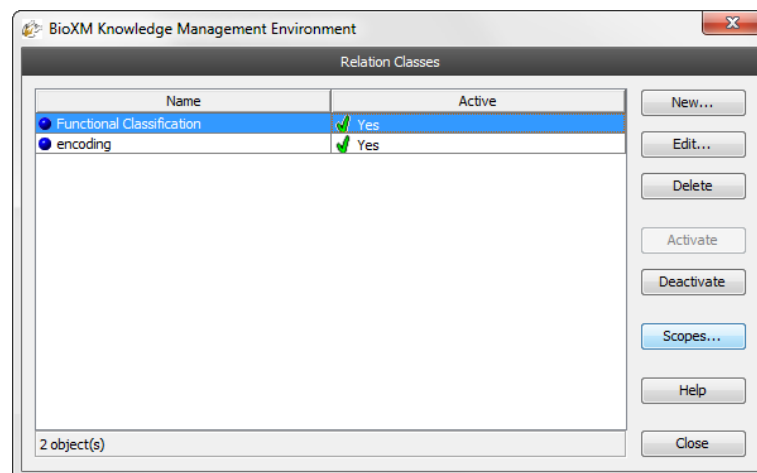


Figure 25. Opening the "Object Type Scopes" dialog via the "Relation Classes" dialog

2. Select a relation class and click the "Scopes..." button to display the "Object Type Scopes" dialog.

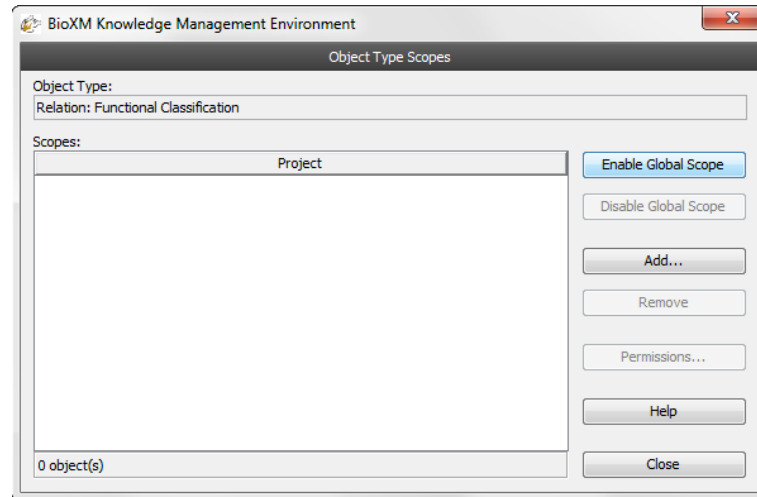



Figure 26. Setting a relation class scope

3. Click the **"Enable Global Scope"** button. After the scope is set, click **"Close"** to close the dialog window.
4. Complete the steps again to set the rest of the scope-capable relations (i.e., "Relation: encoding") to have the "Global Scope".

Upon defining the scopes, the relation classes become available in the "Relations" repository of the project tree (see Figure 16: "Object types of the data model in the project tree").

1.10. Saving the data model layout

Our data model is, in principle, complete. Before we import data into it, we will save the layout for future access.

1. Click the **"Save graph state"** button  (in the top right corner of the window) to display the "Save Graph State" dialog.

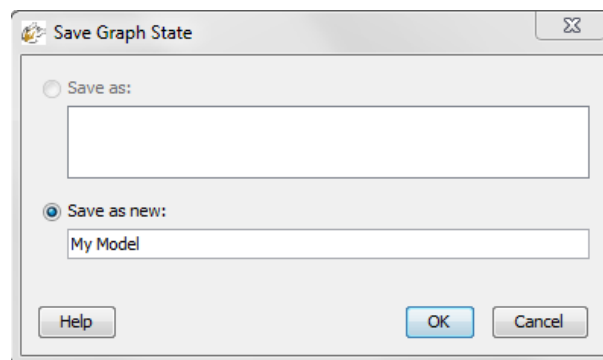


Figure 27. Naming the data model layout

2. Enter a name for the model (e.g., "My Model") in the "Save as new:" field and click the **"OK"** button. The data model layout is saved and can be subsequently selected for display in the data model graph.

1.11. Displaying a saved data model layout

The saved data model layout can be selected for display as follows.

1. Select **"Modeling → Visualize Data Model"** in the main menu to display the "Visualize Data Model" window.

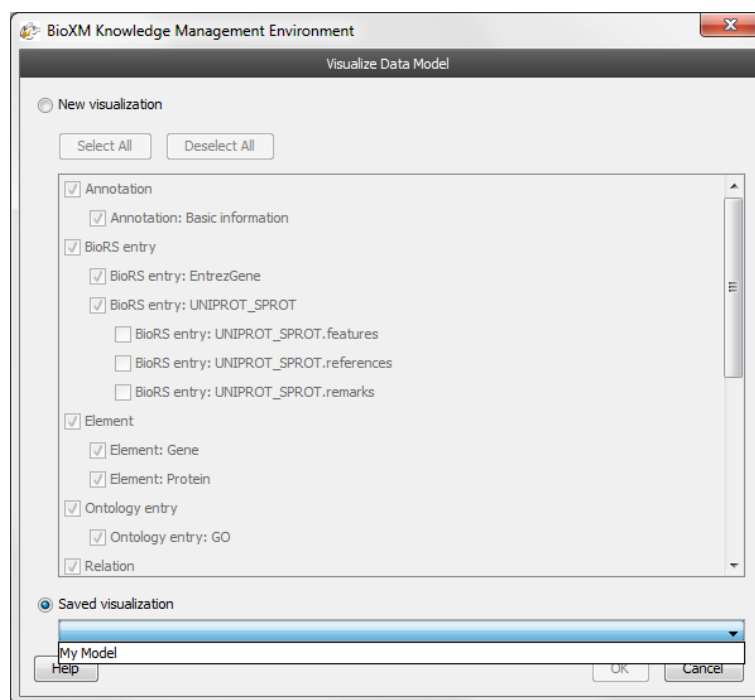


Figure 28. Selecting a saved layout for display

2. Click the "Saved visualization" option and select the "My Model" layout from the drop-down menu. Click "OK" to display the data model graph with the selected layout.

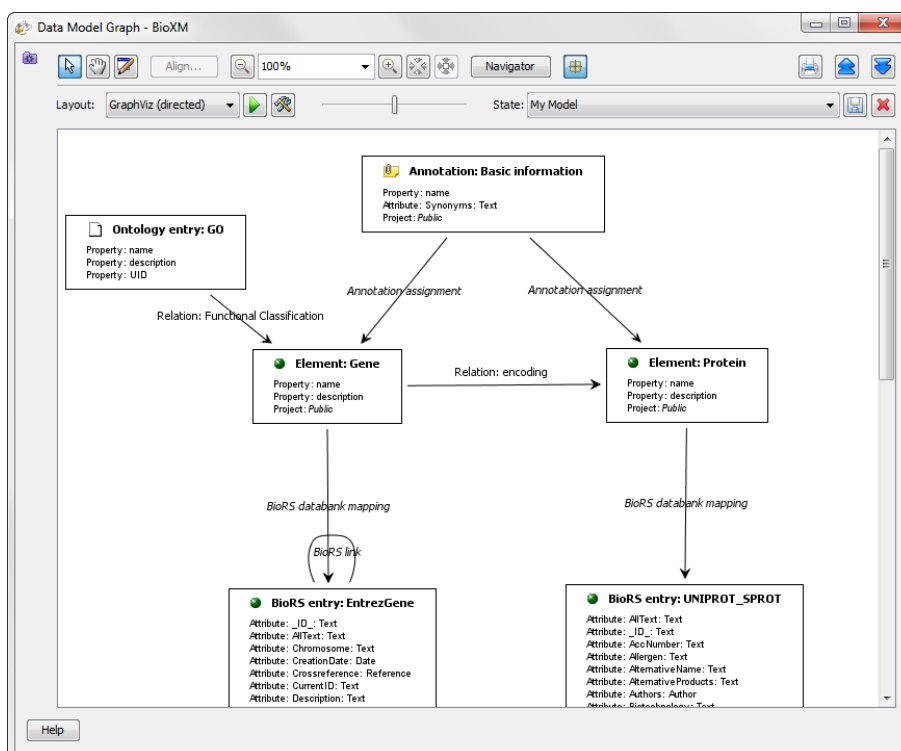


Figure 29. Displaying a saved layout in the data model graph

2. Importing data

Now that we have the basic data model established, we will populate the knowledge network with data and information from external resources.

The BioXM system has a versatile importer for tables of data, which enables users to define the semantic of the table columns and graphically build instruction sets ("scripts") to guide the data import. During the import, information contained in the input data file is transformed according to the semantics of the data model. This mapping process between the defined data model and the input data ensures consistency in the knowledge network.

This section describes importing a table of gene data, creating an import script and saving it for future use. An import "wizard" guides the configuration of the import script. It includes specifying how the data is imported; assigning annotation, external databank entries and ontology entries to the elements; and looking up and creating relations.

2.1. Defining the import

To import the table *Genes.txt*, we will use the "Tabular data import" function, which allows us to specify how data will be uploaded according to the data model. In the following series of steps, only the specified options need to be changed; other options can be left on the default settings.

1. Select "*File* → *Import Table...*" in the main menu to display the first step of the "Import Table Data" wizard (import wizard).
2. Do the following to choose the data source.
 1. Enter the path to the file to be used for import. Alternatively, browse to the location of the file to upload.
 2. Select the type of file for import (e.g., the "Autodetect" option to detect the format automatically).
 3. Click the "**Next**" button to continue to the "Define Physical Layout" step of the import wizard.

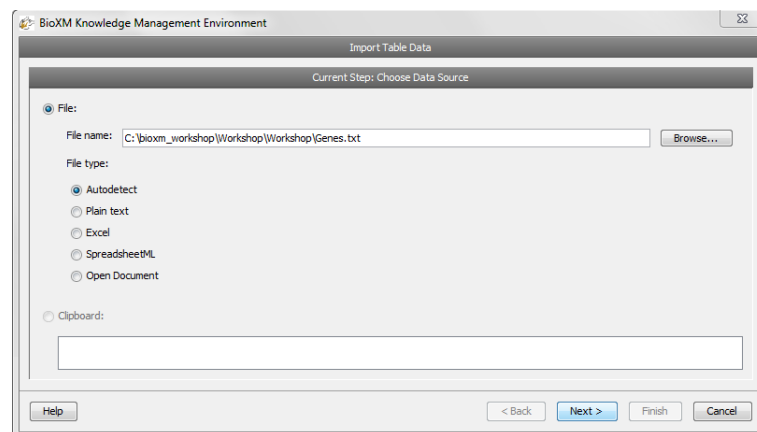


Figure 30. Importing data — choosing the data source

3. Do the following to define the physical layout of the table. A preview of the data is displayed at the bottom of the window.
 1. Under "Columns", click the "Separated columns" radio button. Specify the column separator under "Separator" by selecting the "Preset:" option and "Tab" from the drop-down menu.
 2. Under "Columns" > "Text qualifier" select the "None" radio button.
 3. Under "Header" select "0" lines to skip and click the "Recognize table header" option.
 4. Under "Encoding" select "UTF-8" to accommodate special characters.
 5. Click the "**Next**" button to continue to the "Choose Script Kind" step of the import wizard.

BioXM Knowledge Management Environment

Import Table Data

Current Step: Define Physical Layout

Columns

☒ Separated columns:

Separator: ☒ Preset: **Tab** ☐ Custom: ☐ None

Text qualifier: ☐ Preset: ☐ Custom: ☒ None

☐ Treat consecutive separators as one

☐ Fixed number of columns:

☐ Fixed width columns:

Comma-separated list of column widths, the last may be "*" to take maximum space.

Header

Lines to skip:

☒ Recognize table header

Encoding

Data preview:

	A: Gene Name	B: Synonyms	C: EntrezGene ID	D: GO: Ontology entry Uid
2	15E1.2 [Homo sapiens]	MGC129938;15E1.2;MGC129938...	283459	GO:0017068;GO:0000004;GO:0...
3	76P [Homo sapiens]	GCP4;FLJ14797;GCP4;76P;TUBG...	27229	GO:0000226;GO:0005815;GO:0...
4	A1BG [Homo sapiens]	A1B;ABG;GAB;HYST2477;DKFZp...	1	GO:0016020;GO:0000004;GO:0...
5	A2BP1 [Homo sapiens]	FOX1;HRNBP1;FOX1;HRNBP1;A2...	54715	GO:0000166;GO:0003723;GO:0...
6	A2M [Homo sapiens]	dkfz779b086;alpha-2-macroglo...	2	GO:0004867;GO:0005576;GO:0...
7	A2ML1 [Homo sapiens]	CPAMD9;FLJ16045;FLJ25179;FL...	144568	GO:0004866
8	A3GALT2 [Homo sapiens]	A3GALT2;a 1,3-galactosyltransf...	127550	GO:0005975;GO:0016020;GO:0...
9	A4GALT [Homo sapiens]	P1;PK;A14GALT;A4GALT1;PK;A4...	53947	GO:0005624;GO:0005795;GO:0...

Figure 31. Importing data — defining the physical layout

4. Select the "New script" option and click the **Next** button to continue to the "Define Tab Import Script" step of the import wizard.

BioXM Knowledge Management Environment

Import Table Data

Current Step: Choose Script Kind

☒ New script
Create the new script from scratch.

☐ Existing script
Choose a script stored in the database.

Data preview:

	A: Gene Name	B: Synonyms	C: EntrezGene ID	D: GO: Ontology entry Uid
2	15E1.2 [Homo sapiens]	MGC129938;15E1.2;MGC129938...	283459	GO:0017068;GO:0000004;GO:0...
3	76P [Homo sapiens]	GCP4;FLJ14797;GCP4;76P;TUBG...	27229	GO:0000226;GO:0005815;GO:0...
4	A1BG [Homo sapiens]	A1B;ABG;GAB;HYST2477;DKFZp...	1	GO:0016020;GO:0000004;GO:0...
5	A2BP1 [Homo sapiens]	FOX1;HRNBP1;FOX1;HRNBP1;A2...	54715	GO:0000166;GO:0003723;GO:0...
6	A2M [Homo sapiens]	dkfz779b086;alpha-2-macroglo...	2	GO:0004867;GO:0005576;GO:0...
7	A2ML1 [Homo sapiens]	CPAMD9;FLJ16045;FLJ25179;FL...	144568	GO:0004866
8	A3GALT2 [Homo sapiens]	A3GALT2;a 1,3-galactosyltransf...	127550	GO:0005975;GO:0016020;GO:0...
9	A4GALT [Homo sapiens]	P1;PK;A14GALT;A4GALT1;PK;A4...	53947	GO:0005624;GO:0005795;GO:0...
10	A4GNT [Homo sapiens]	loc51146;a4gnt;mgc149493;alph...	51146	GO:0016757;GO:0016021;GO:0...
11	AAAS [Homo sapiens]	AAA;AAASb;GL003;ADRACALA;...	8086	GO:0005554;GO:0005643;GO:0...
12	AACS [Homo sapiens]	SUR-5;FI112389;FI141251;SUR...	65985	GO:0003824;GO:0003987;GO:0...

Figure 32. Importing data — choosing the kind of script

After the script is defined and saved, it will be stored in the database. During subsequent data import, it can be used by selecting the "Existing script" option.

2.2. Configuring the tab import script

The next series of steps configures the tab import script used to import the *Genes.txt* data. A workflow of several import operations is defined. Each import operation is selected from the "Available import operations" panel on the left. The defined workflow is displayed in the "Tab import script" panel in the middle. Depending on the item selected in the middle panel, a dialog for specifying the necessary information is displayed in the right panel.

Note, that this kind of three-panel layout is often used in the BioXM user interface. An option is selected in the left panel, listed in the middle panel and defined in the right panel.

In the following series of steps, only the specified options need to be changed; other options can be left on the default settings.

- Under "Available import operations" select "Lookup or create element" and click the "Add>>" button. Options for the import operation will be displayed under "Tab import script". Click each option listed in the table below to display the settings in the right panel. After selecting the listed settings, click the "Apply" button.

Table 1. "Look up or create element" operation

Option selected in the "Tab import script" panel	Settings in right panel
Name	Select the "Take from column" option and "A: Gene Name" from the drop-down menu.
Type	Select the "Use constant value" option and "Gene" from the drop-down menu.
Create in project	Select the "Default for Element Type" radio button. The project will be set to the default for Gene elements, i.e., the "Public" project.

The defined operation is shown below.

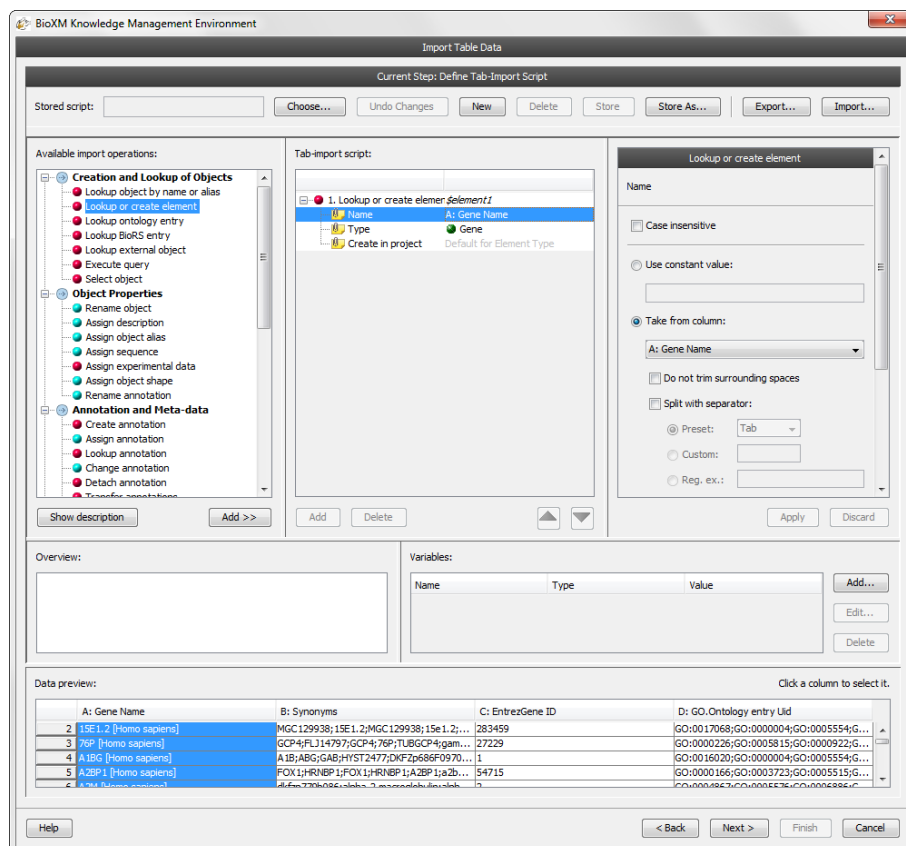


Figure 33. Importing data — tab import script "Lookup or create element" operation

2. Under "Available import operations" select "Create annotation" and click the **"Add>>"** button. Options for the import operation will be displayed under "Tab import script". Click each option listed in the table below to display the settings in the right panel. After selecting the listed settings, click the **"Apply"** button.

Table 2. "Create annotation" operation

Option selected in the "Tab import script" panel	Settings in right panel
Object	Select the "\$element1" option from the drop-down menu.
Name	Use the default settings. A name is optional.
Form	Select the "Basic information" annotation form from the drop-down menu.
Overwrite	Check the "Overwrite single anonymous" check box.
Create in project	Select the "Default for Annotation Form" radio button. The project will be set to the default project for the annotation form, i.e., the "Public" project.
Synonyms	<p>Set several options:</p> <ul style="list-style-type: none"> • Check the "Exclude duplicated values" check box. • Check the "Add to existing values" check box. • Select the "Take from column:" radio button and "B: Synonyms" from the drop-down menu. • Check the "Split with separator" check box, select the "Preset" radio button, and select the semi-colon ";" from the drop-down menu. • Click the "Edit" link next to "Empty/invalid values processing". A dialog will open. Select the "Skip" radio button for both "Empty values" and "Invalid values" and click the "OK" button.

The defined operation is shown below.

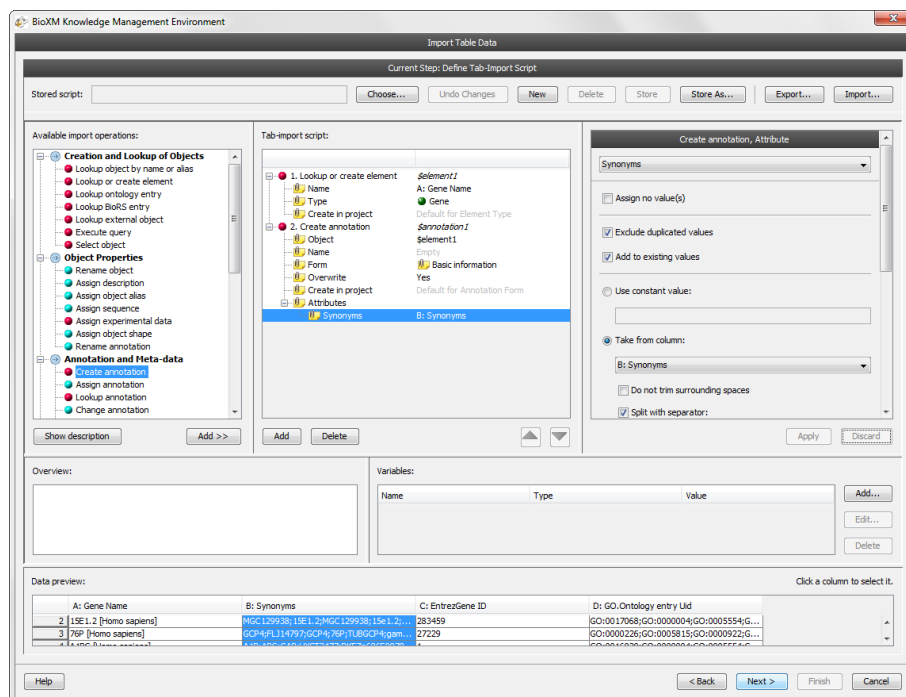


Figure 34. Importing data — tab import script "Create annotation" operation

3. Under "Available import operations" select "Lookup and assign BioRS" and click the **"Add>>"** button. Options for the import operation will be displayed under "Tab import script". Click each option listed in the

table below to display the settings in the right panel. After selecting the listed settings, click the **"Apply"** button.

Table 3. "Lookup and assign BioRS" operation

Option selected in the "Tab import script" panel	Settings in right panel
Object	Select the "\$element1" option from the drop-down menu.
Databank	Select "Use constant value" and "EntrezGene" from the drop-down menu.
Element name	Select "Use constant value" and "_ID_" from the drop-down menu. ("_ID_" is the primary key in the EntrezGene databank.)
Element value	Set several options: <ul style="list-style-type: none"> Select the "Take from column:" radio button and "C: EntrezGene ID" from the drop-down menu. Check the "Split with separator" check box, select the "Preset" radio button and select the semi-colon ";" from the drop-down menu. Click the "Edit" link next to "Empty/invalid values processing". A dialog will open. Select the "Skip" radio button for both "Empty values" and "Invalid values" and click the "OK" button.
Skip lookup by _ID_	Check the "Assume entry exists when looking up by _ID_" check box. (Setting the "Skip lookup by _ID_" option to "Yes" will increase the speed of the import because the BioXM system will skip creating a connection to the BioRS databank to check if the entry exists.)

The defined operation is shown below.

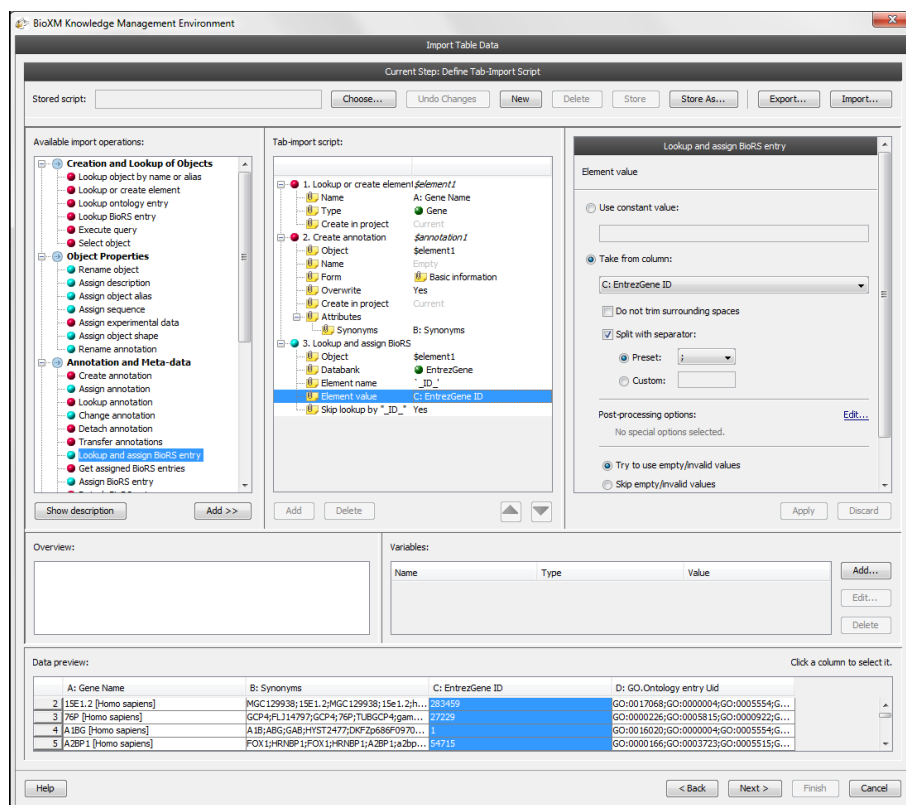


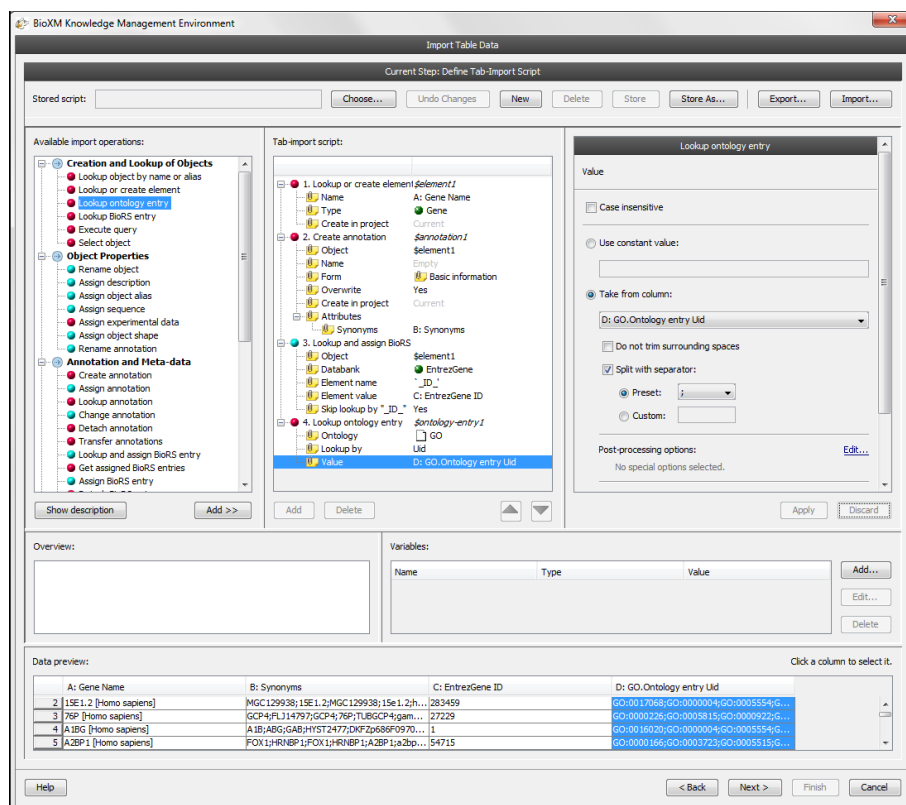
Figure 35. Importing data — tab import script "Lookup and assign BioRS" operation

- Under "Available import operations" select "Lookup ontology entry" and click the **"Add>>"** button. Options for the import operation will be displayed under "Tab import script". Click each option listed in the table below to display the settings in the right panel. After selecting the listed settings, click the **"Apply"** button.

Table 4. "Lookup ontology entry " operation

Option selected in the "Tab import script" panel	Settings in right panel
Ontology	Select "Use constant value" and "GO" from the drop-down menu.
Lookup by	Select the "Uid" radio button to look entries up by a unique identifier (UID).
Value	<p>Set several options:</p> <ul style="list-style-type: none"> Select the "Take from column:" radio button and "<i>D:GO.Ontology entry Uid</i>" from the drop-down menu. Check the "Split with separator" check box, select the "Preset" radio button and select the semi-colon ";" from the drop-down menu. Click the "Edit" link next to "Empty/invalid values processing". A dialog will open. Select the "Skip" radio button for both "Empty values" and "Invalid values" and click the "OK" button.

The defined operation is shown below.

**Figure 36. Importing data — tab import script "Lookup ontology entry" operation**

- Under "Available import operations" select "Lookup or create relation" and click the "Add>>" button. Options for the import operation will be displayed under "Tab import script". Click each option listed in the table below to display the settings in the right panel. After selecting the listed settings, click the "Apply" button.

Table 5. "Lookup or create relation" operation

Option selected in the "Tab import script" panel	Settings in right panel
Relation class	Select the "Use constant value" option and " <i>Functional Classification</i> " from the drop-down menu.

Option selected in the "Tab import script" panel	Settings in right panel
Source	Select the "Use result variable" option and "\$ontology-entry1" from the drop-down menu.
Target	Select the "Use result variable" option and "\$element1" from the drop-down menu.
Create in project	Select the "Default for Relation Class" radio button. The project will be set to the default project for the relation class, i.e., the "Public" project.

The defined operation is shown below.

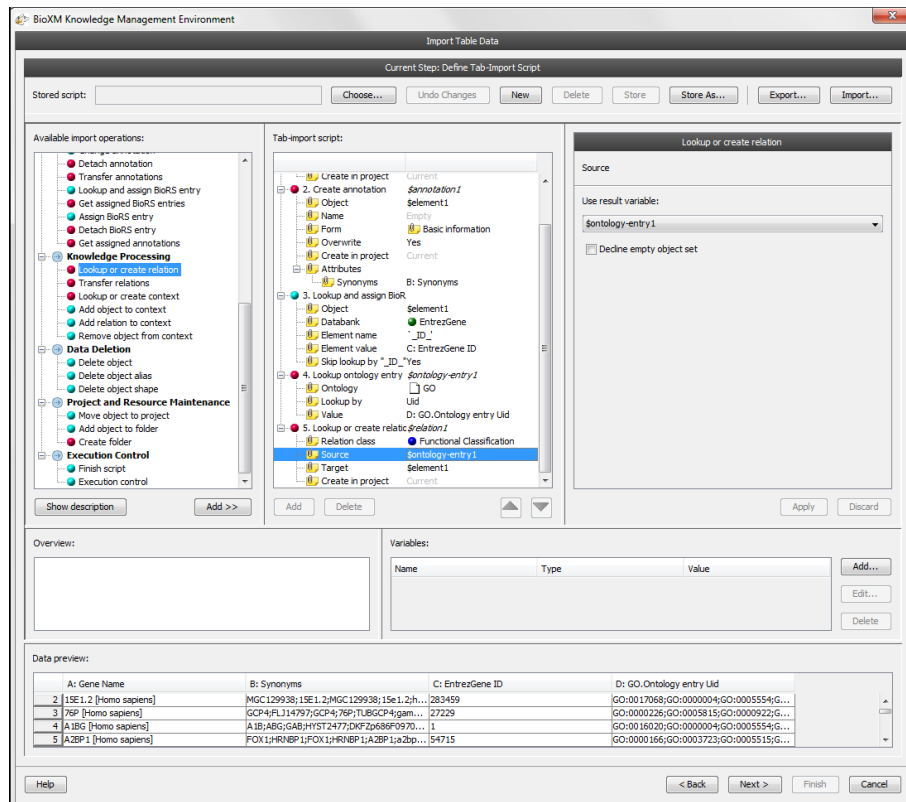


Figure 37. Importing data — tab import script "Lookup or create relation" operation

- Before continuing, we will store the import script. Click the **"Store as..."** button at the top of the import wizard. Enter a name for the tab-import script in the dialog and click the **"OK"** button to return to the wizard.

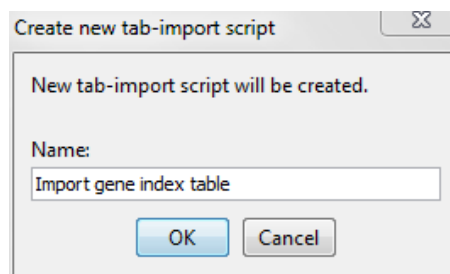


Figure 38. Importing data — storing the import script

Click the **"Next>"** button in the import wizard to continue to the "Choose Processing Policy" step.

2.3. Simulating the import

First, we will simulate the import using the first 100 items to make sure the import script works as needed. Then we will import the entire table.

BioXM Knowledge Management Environment

Import Table Data

Current Step: Choose Processing Policy

☐ Allow partial import
Commit changes for errorless import operations by small portions.

☐ Allow complete import only
Do not commit any changes if any errors were found.

☒ Simulate import
Do not commit any changes even on successful import.

☐ Stop after the specified number of errors:

☒ Process only lines:

 Comma-separated list of ranges each in the form "from-to" (either end may be omitted). Example: "-10, 20-30, 40, 50-".

☒ Produce import log
 Record all import operation activity for each table row.

Data preview:

	A: Gene Name	B: Synonyms	C: EntrezGene ID	D: GO.Ontology entry Uid
2	15E1.2 [Homo sapiens]	MGC129938;15E1.2;MGC129938;15e1.2;h...	283459	GO:0006450
3	76P [Homo sapiens]	GCP4;FLJ14797;GCP4;76P;TUBGCP4;gam...	27229	GO:0000226;GO:0005815;GO:000922;G...
4	A1BG [Homo sapiens]	A1B;ABG;GAB;HYST2477;DKFZp686F0970...	1	GO:0016020;GO:0005576
5	A2BP1 [Homo sapiens]	FOX1;HRNBP1;FOX1;HRNBP1;A2BP1;a2bp...	54715	GO:0000166;GO:0003723;GO:0005515;G...
6	A2M [Homo sapiens]	dkfzp779b086;alpha-2-macroglobulin;alph...	2	GO:0004867;GO:0005576;GO:0006886;G...
7	A2ML1 [Homo sapiens]	CPAMD9;FLJ16045;FLJ25179;FLJ39129;FL...	144568	GO:0004866
8	A3GALT2 [Homo sapiens]	A3GALT2;a1,3-galactosyltransferase 2 (s...	127550	GO:0005975;GO:0016020;GO:0016758

Figure 39. Importing data — choosing a processing policy to simulate the import

1. Click the "Simulate import" radio button.
2. Click the "Process only lines:" check box and set a number of lines to process (e.g., "-100" to simulate the first 100 lines) or leave the check box empty to simulate the entire import.
3. Click the "Produce import log" check box to record all import operation activity for each line.
4. Click the **Next** button to continue to the "Import Data" step of the wizard.

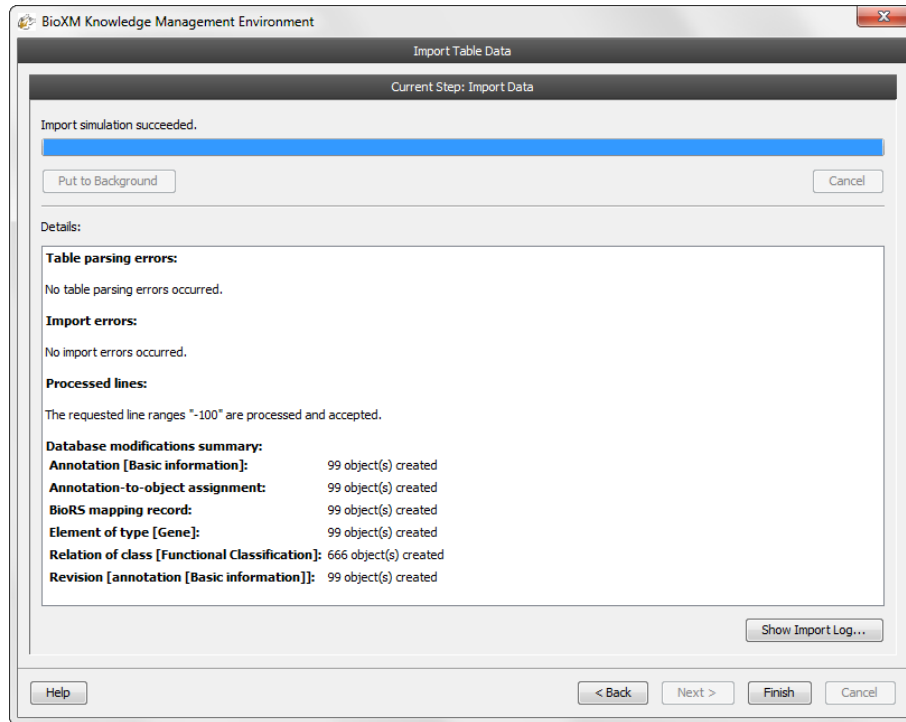


Figure 40. Importing data — simulating the import

The import simulation may take some time, but you can continue working with the BioXM system as the import is processed by clicking the **"Put to background"** button. To display the task again, select *"View → Show Background Task Manager"* in the main menu. The "Background Task Manager" window will be displayed. Click the task and the **"Task Details..."** button to display the task.

5. If there are no problems upon completion of the simulation, we can proceed to the actual data import by clicking the **"Back"** button. See Section 2.5: "Completing the import".

If there are errors reported see Section 2.4: "Trouble-shooting the import".

2.4. Trouble-shooting the import

The section lists some typical errors encountered when importing and how to overcome them.

2.4.1. Error: Insufficient privileges

If the following type of error is displayed, check that the correct scopes are set for all scope-capable objects and relations in the data model.

```
ERROR: Insufficient privileges
```

See Section 1.8: "Defining object type scopes" and Section 1.9: "Defining relation class scopes".

2.4.2. Error: Entry not found

If an entry is not found and a variable cannot be defined, the following type of error will be displayed.

```
Table parsing errors: No table parsing errors occurred.
Import errors:
Line 2: ERROR: Ontology entry with uid `GO:0017068' not found.
Line 2: ERROR: Ontology entry with uid `GO:0000004' not found.
Line 2: ERROR: Ontology entry with uid `GO:0005554' not found.
Line 2: ERROR: Ontology entry with uid `GO:0008372' not found.
Line 2: ERROR: Variable `$ontology-entry1' is not defined.
```

```

Line 4: ERROR: Ontology entry with uid `GO:0000004' not found.
Line 4: ERROR: Ontology entry with uid `GO:0005554' not found.
Line 4: ERROR: Variable `$ontology-entry1' is not defined.
Processed lines: The requested line ranges "-10" are rejected
                  and does not influence database modifications.
Database modifications summary: No database modifications were performed.

```

If the "Allow partial import" option is selected, such errors will be ignored during the import. See Section 2.5: "Completing the import".

2.5. Completing the import

If there are no problems upon simulating the import, we can proceed to the actual data import.

1. Open the "Choose processing policy" step of the import wizard.

In the import wizard, click the **"Back"** button. Alternatively, start a new import wizard by selecting *"File → Import Table..."* in the main menu and using the existing "Import gene index table" script. Click the **"Next"** button until the "Choose processing policy" step of the wizard is displayed.

2. Choose a processing policy to perform the import.

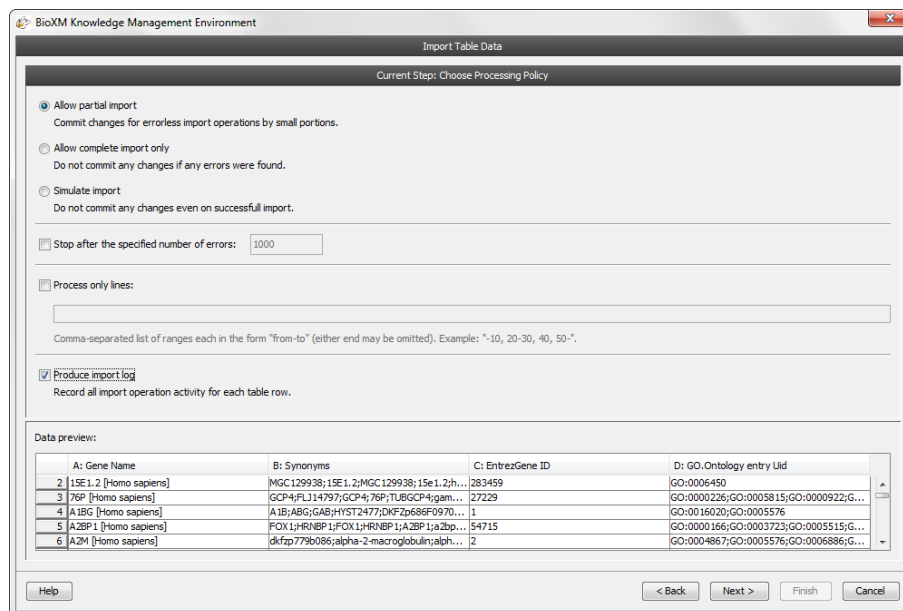


Figure 41. Importing data — choosing a processing policy to perform the import

Do the following in this step of the import wizard:

1. Click the "Allow partial import" radio button.
2. Clear the "Process only lines:" check box.
3. Click the "Produce import log" check box to record all import operation activity for each line (optional).
4. Click the **"Next"** button to continue to the "Import Data" step of the wizard.

The "Allow partial import" option sets the BioXM system to process the import operations by small portions (chunks). The system automatically optimizes the number of rows processed based on network capabilities and import speed. Partial import allows multiple imports to run simultaneously — each allowing one chunk at a time into the queue. If the **"Cancel"** button is clicked during the import, the import is not stopped immediately, but after completing the current chunk. In addition, some import errors are ignored (e.g., "Entry not found" errors).

The "Allow complete import only" option sets the BioXM system to import the entire table at once, not in chunks. Other import scripts in the queue will wait until the entire upload has been processed.

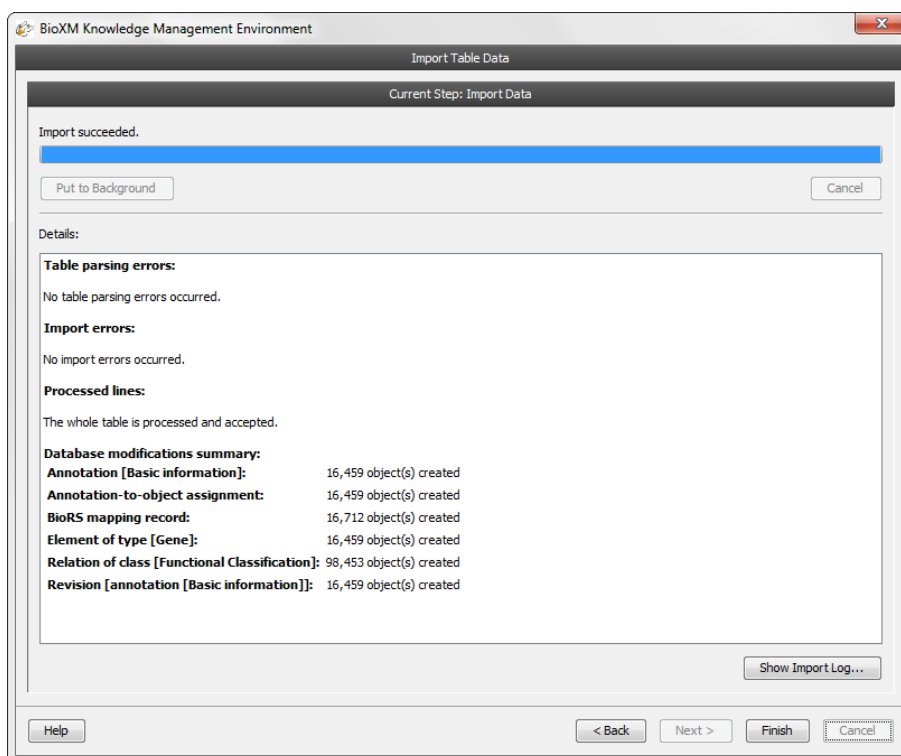


Figure 42. Importing data — completing the import

The import may take some time, but you can continue working with the BioXM system as the import is processed by clicking the **"Put to background"** button. To display the task again, select *"View → Show Background Task Manager"* in the main menu. The "Background Task Manager" window will be displayed. Click the task and the **"Task Details..."** button to display the task.

3. Finishing the data import

Click the **"Finish"** button to close the import wizard. The imported elements (genes) will be displayed in the default "Element Type View".

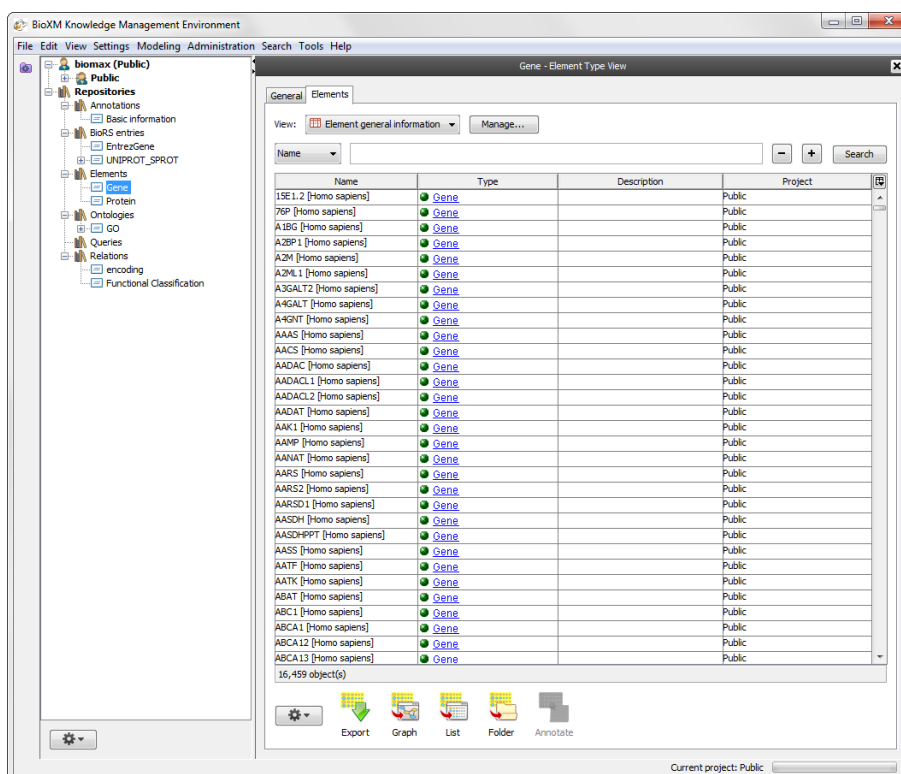


Figure 43. Displaying the gene list

The "Element general information" view is the built-in, default view for genes. In Section 3.1: "Creating a view", we will create a view for genes which is tailored for use in the "gene index" use case.

3. Preparing views and queries

In this section we will prepare the system for use by creating views, queries and smart folders. This will allow us to tailor how the information in the gene index knowledge network is presented so we can query the knowledge network, explore the network graph and report the query results as specifically needed. We will create a gene list view and smart folders tailored to our use case.

3.1. Creating a view

Views display a selection of information about selected objects. Information displayed in the view can be taken from the object properties (such as name and description) or from other associated objects. For each element, there is always one built-in view, e.g., "Element general information", which shows the default properties available for the object (see Figure 43: "Displaying the gene list"). Initially, it is set as the default view; however, additional views can be created to address specific needs and set as the default view.

We will create a new view so the gene list displays the information most relevant to this use case.

1. To create a new view, select "*Administration* → *Views...*". (This item will be enabled only for users with the appropriate privileges. For more information about privileges, see the *BioXM User Manual*.) Alternatively, in any open view, click the "**Manage...**" button next to the name of the view. The "Views" dialog is displayed.

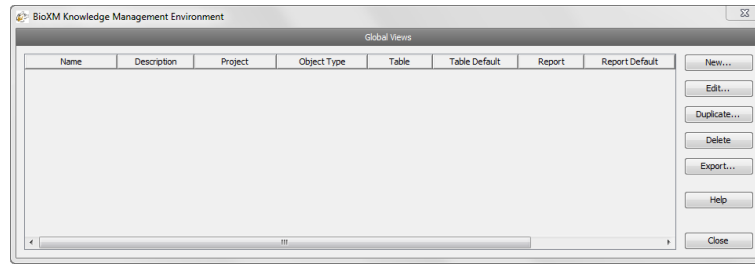


Figure 44. Creating a view — the "Views" dialog

- Click the "New..." button to display the "New View" dialog (see Figure 45, "Creating a view — "General" tab").
- Define the following information for the new view in the "General" tab.

Table 6. "General" tab options

Option in the "General" tab	Settings
Name	Enter "Gene list view" in the field.
Allowed types	Select the type of object for which the view will be available (e.g., kind "Element" and element type "Gene") from the drop-down menus.
Description	Enter a short description of the view (optional).
Project	Select the "Public" project.
Allowed for table	Select the "Allowed for table" and "Use as default for table" options.
Allowed for report	Select the "Allowed for report" and "Use as default for report" options.

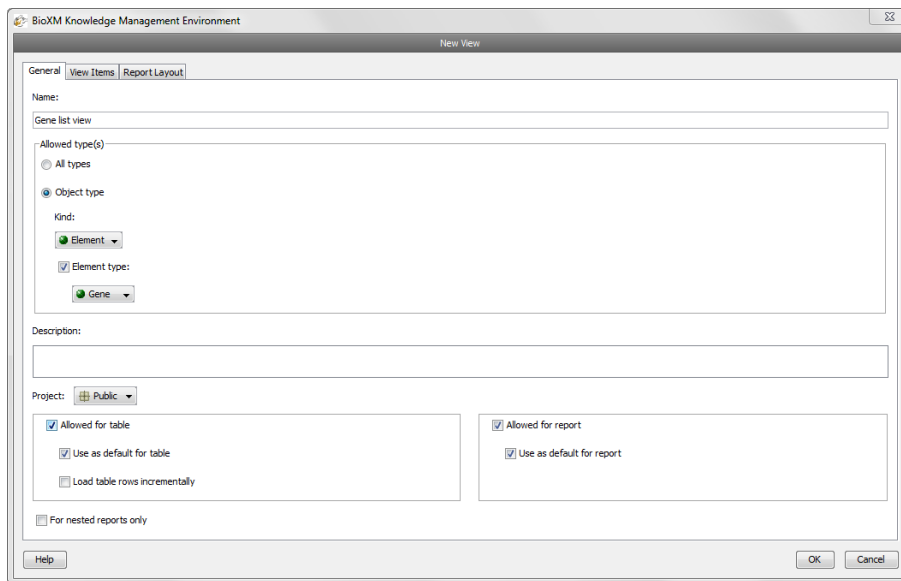
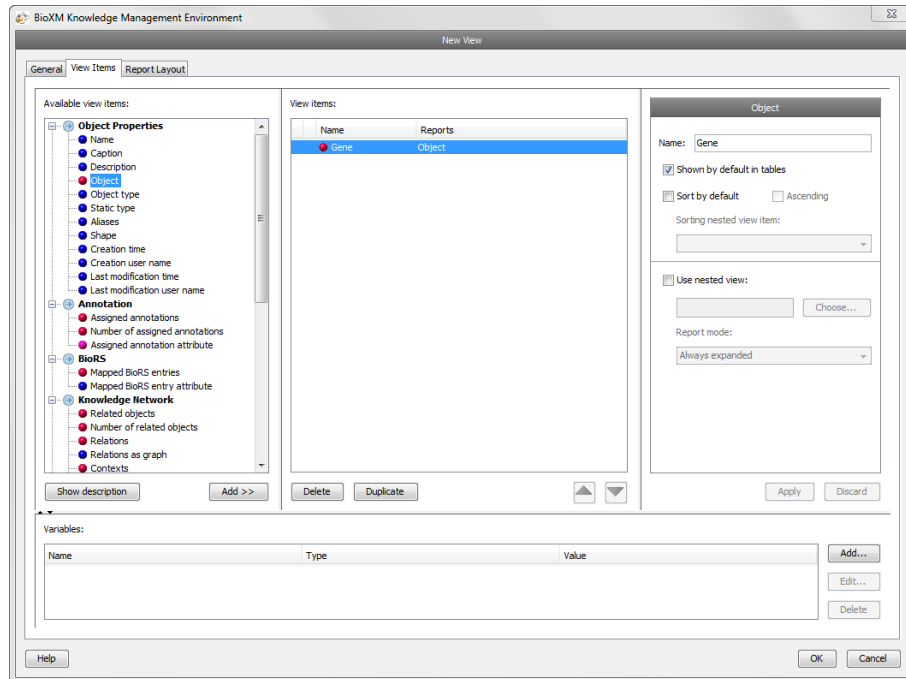


Figure 45. Creating a view — "General" tab

- Click the "View items" tab. The "View Items" interface (see Figure 46: "Creating a view — "View Items" tab "Object" definition") is similar to the import wizard with three panels. Each view item is selected from the "Available view items" panel on the left. The added item is displayed in the "View items" panel in the middle. Depending on the item selected in the middle panel, a dialog for specifying the necessary information appears in the right panel. The view items will become the columns of the table in the order they are listed in the middle panel.
- In the "Available view items" panel, under "Object Properties" select the "Object" option and click the "Add>>" button. Define the following information in the right panel and click the "Apply" button.

Table 7. "View Items" tab "Object" definition

Option in the "View Items" panel	Settings
Name	Enter "Gene" in the field.
Shown by default in tables	Select the "Shown by default in tables" option.

**Figure 46. Creating a view — "View Items" tab "Object" definition**

- In the "Available view items" panel, under "BioRS" select the "BioRS mapped BioRS entries" option and click the "Add>>" button. Define the following information in the panel on the right and click the "Apply" button.

Table 8. "View Items" tab "Mapped BioRS entries" definition

Option in the "View Items" panel	Settings
Name	Enter "EntrezGene" in the field.
Shown by default in tables	Select the "Shown by default in tables" option.
BioRS databank	Select the "BioRS databank" option and "EntrezGene" from the drop-down menu.

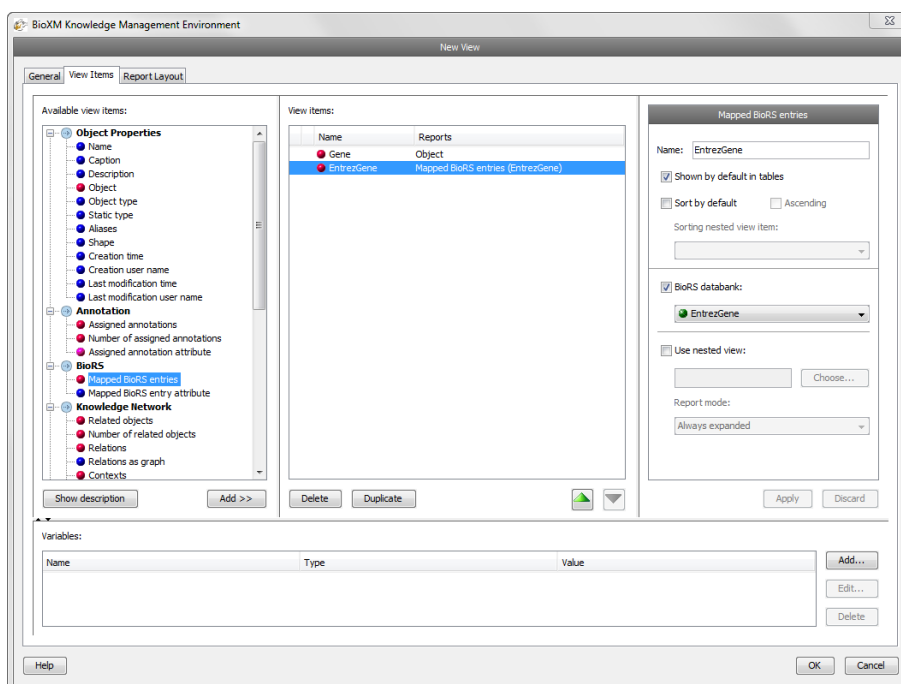


Figure 47. Creating a view — "View Items" tab "Mapped BioRS entries" definition

7. In the "Available view items" panel, under "BioRS" select the "mapped BioRS entry attribute" option and click the "Add>>" button. Define the following information in the panel on the right and click the "Apply" button.

Table 9. "View Items" tab "Mapped BioRS entry attribute" definition

Option in the "General" tab	Settings
Name	Enter "Chromosome" in the field.
Shown by default in tables	Select the "Shown by default in tables" option.
Databank	Select "EntrezGene" from the drop-down menu.
Attribute	Select "Chromosome" from the drop-down menu.

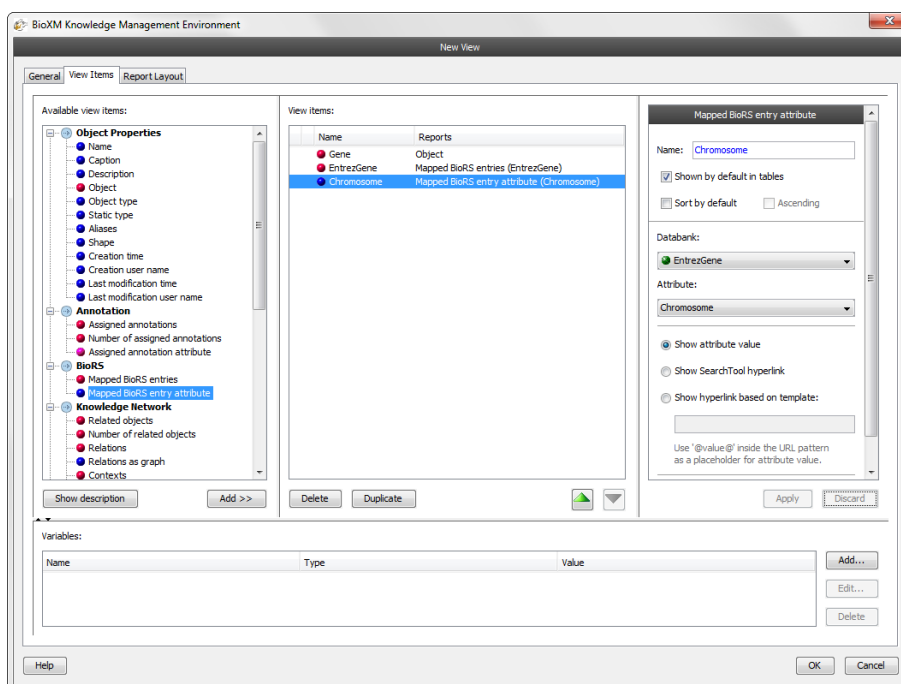


Figure 48. Creating a view — "View Items" tab "Mapped BioRS entry attribute" definition

8. In the "Available view items" panel, under "Annotation" select the "Assigned annotation attribute" option and click the **"Add>>"** button. Define the following information in the panel on the right and click the **"Apply"** button.

Table 10. "View Items" tab "Assigned annotation attribute" definition

Option in the "General" tab	Settings
Name	Enter "Synonym" in the field.
Shown by default in tables	Select the "Shown by default in tables" option.
Annotation form	Select " <i>Basic information</i> " from the drop-down menu.
Attribute	Select " <i>Synonym</i> " from the drop-down menu.

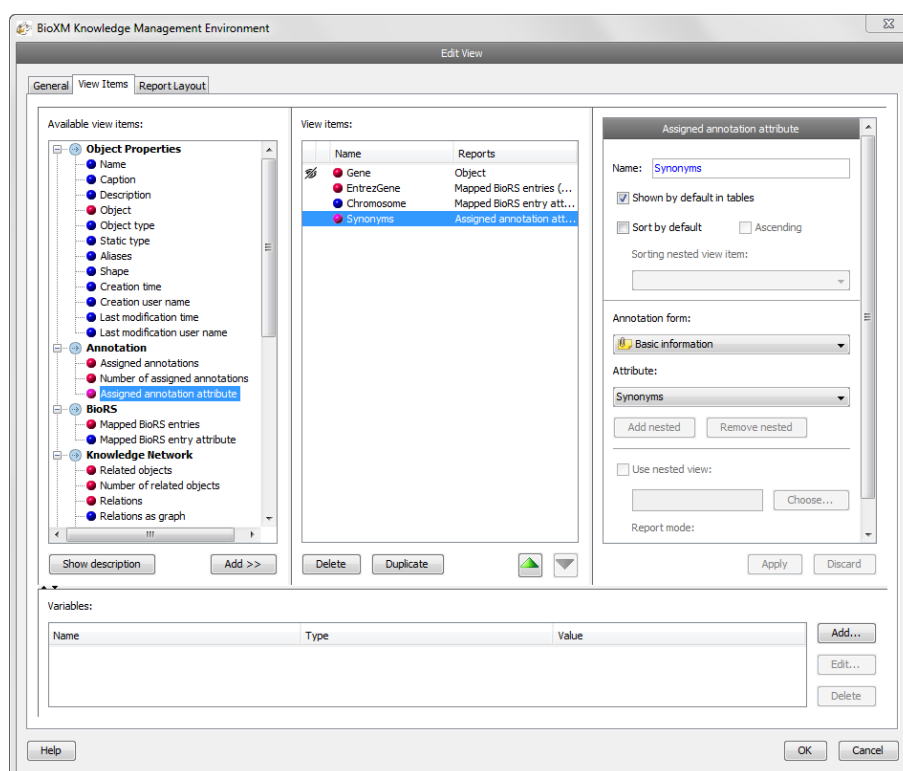


Figure 49. Creating a view — "View Items" tab "Assigned annotation attribute" definition

9. In the "Available view items" panel, under "Knowledge Network" select the "Related objects" option and click the "Add>>" button. Define the following information in the panel on the right and click the "Apply" button.

Table 11. "View Items" tab "Related objects" definition

Option in the "General" tab	Settings
Name	Enter "GO" in the field
Shown by default in tables	Select the "Shown by default in tables" option.
Related object is	Select the "Source or target" option.
Relation class	Click the check box and select " <i>Functional Classification</i> " from the drop-down menu.
Related object type	Select the "Related object type" option. Under "Kind" select " <i>Ontology entry</i> " from the drop-down menu. Under "Ontology" select "GO" from the drop-down menu.

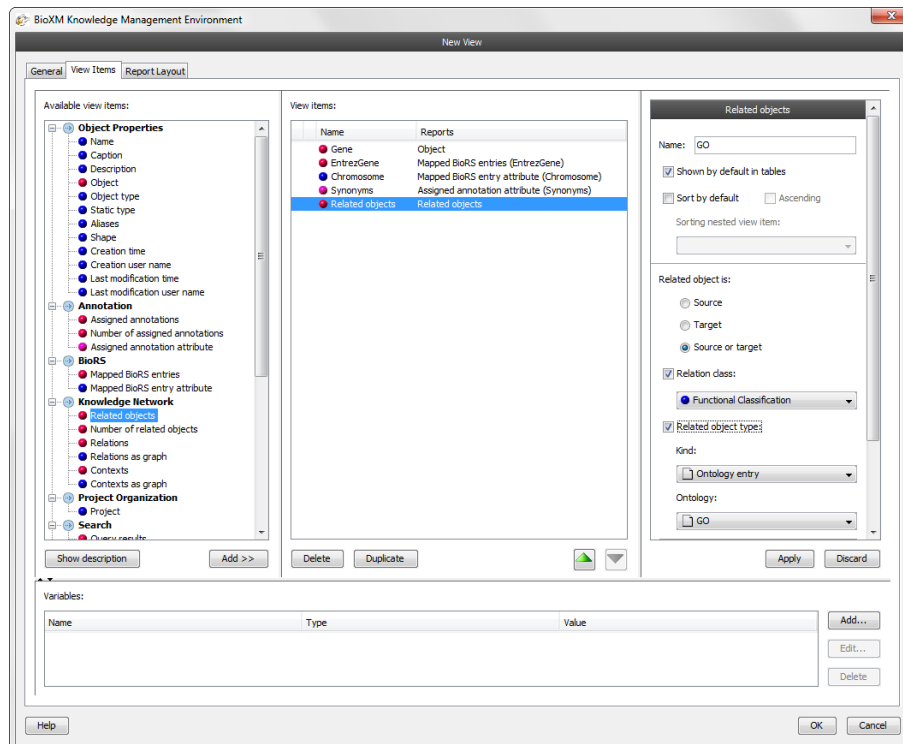



Figure 50. Creating a view — "View Items" tab "Related objects" definition

10. Before closing the dialog, we will reorder the view items so the "Synonyms" are shown in the second column of the "Gene list view" table. Select the "Synonyms" item in the middle panel and click the arrow up button  to put it in the second position in the panel. The view items defined become the columns of the table in the order they are listed in the middle panel.

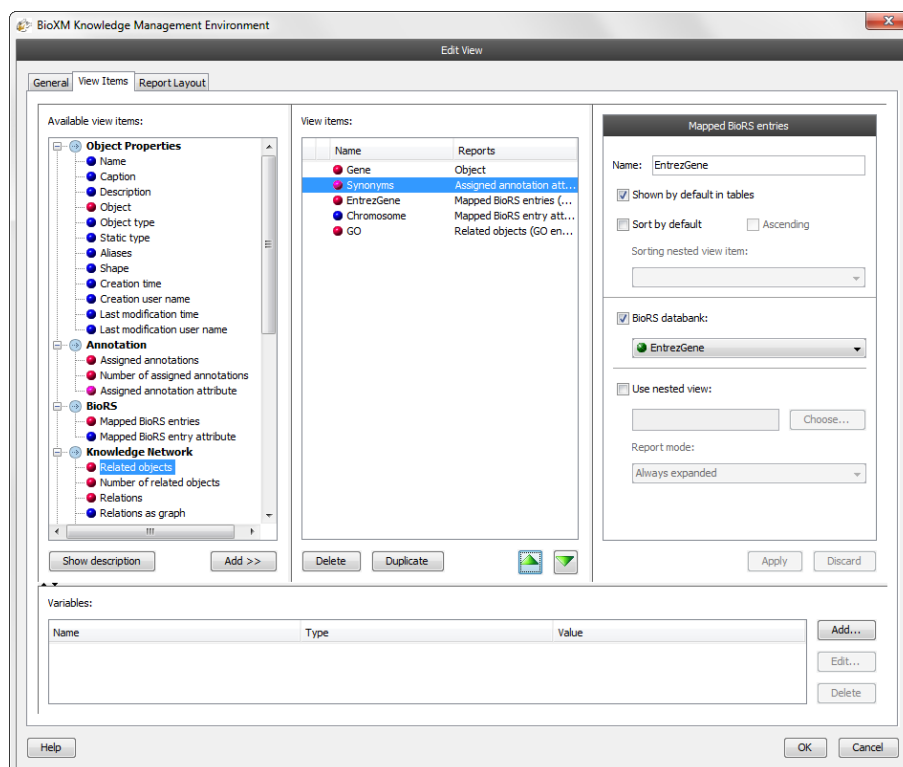


Figure 51. Creating a view — reordering the view items

11. Click the "OK" button to close the dialog. In the "Global Views" dialog, click the "Close" button.

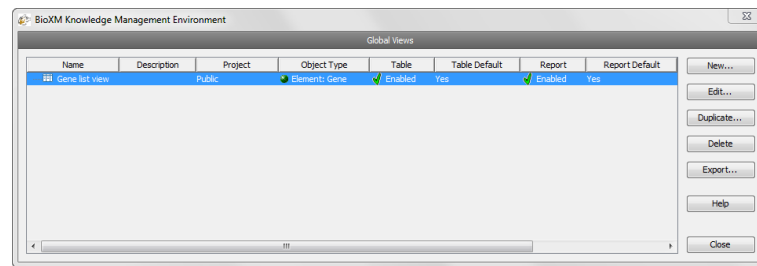


Figure 52. "Global Views" dialog

3.2. Displaying the view

To display the new view, select "Gene list view" from the "View" drop-down menu in the "Gene" element window.

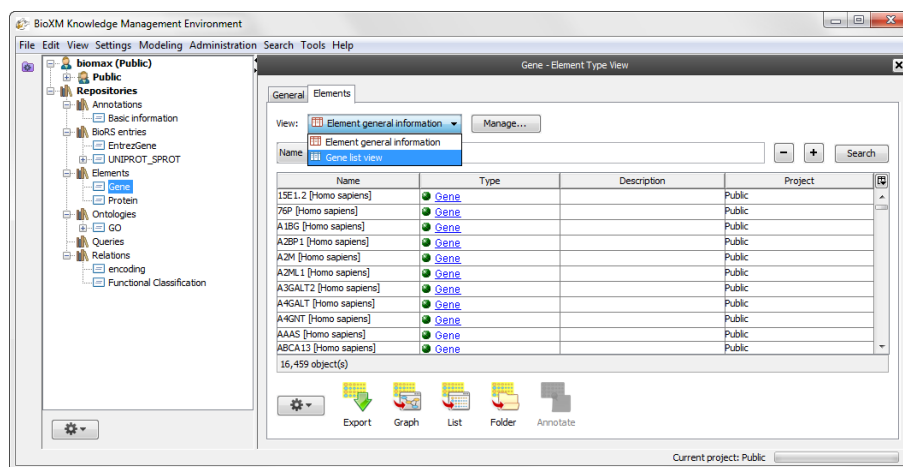


Figure 53. "Element general information" view — selecting a new view

In the view, the columns can be sorted by clicking any column header (e.g., "Chromosome"). Columns can be selected to be displayed or not by clicking the table icon in the top right corner of the table.

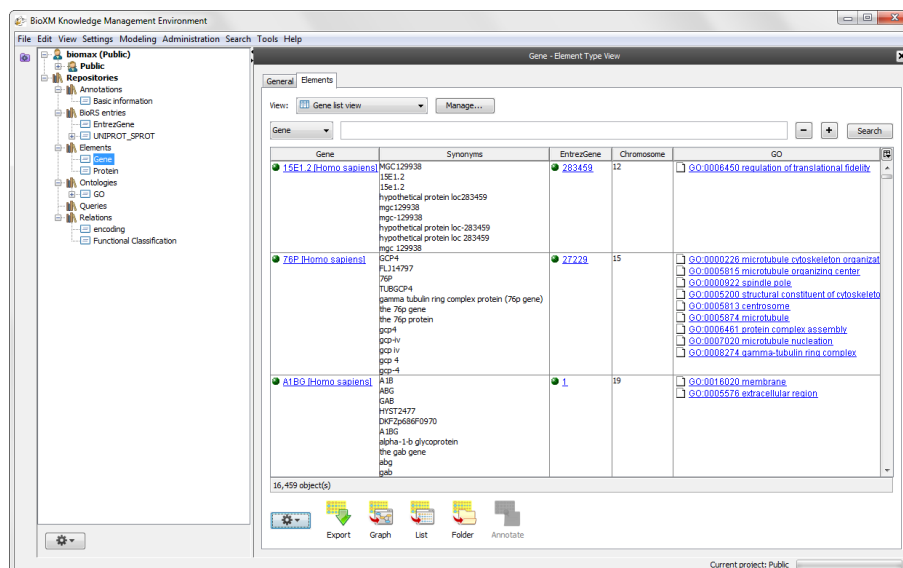


Figure 54. Displaying the "Gene list view"

The appearance of the view is automatically saved for each user and will be the same the next time the view is displayed.

3.3. Creating a query

Next we will create a query to answer a specific scientific question or perform a specific task in our use case. In the first example we will create a query to find all signal transduction genes in the knowledge network. In the second example we will create a general query to find genes by function.

Queries can be easily defined within the BioXM system using a graphical user interface which is similar to the import wizard. The query builder features a query language similar to a natural language and can support complex search tasks. A query can be stored in the query repository for later reuse. A query can also be saved as a smart folder within a project folder. Each time the smart folder is opened the query is performed, ensuring up-to-date information with no maintenance effort.

1. Select "Search → Find by advanced query" in the main menu.

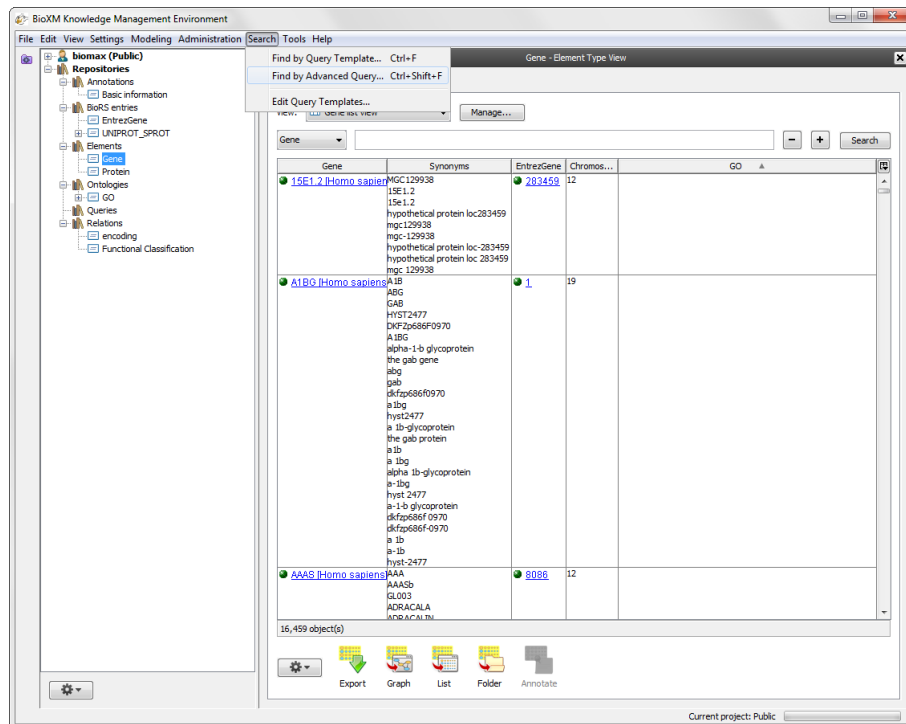


Figure 55. Creating a query — accessing the query wizard

The "Find by advanced query" wizard will be displayed. It is similar to the import wizard with three panels. Query criteria are selected from the "Criteria available" panel on the left. The added criteria are displayed in the "Object to find" panel in the middle. Depending on the criteria selected in the middle panel, a dialog for specifying the necessary information appears in the right panel.

2. We want to search for genes involved in signal transduction so we will perform a search for genes that are classified by the GO ontology entry "signal transduction".

In the "Criteria available" panel under "Object Selection" open "is an element" and select "is a gene". Click the "Add>>" button to list it in the "Object to find" panel. Nothing needs to be changed in the right panel.

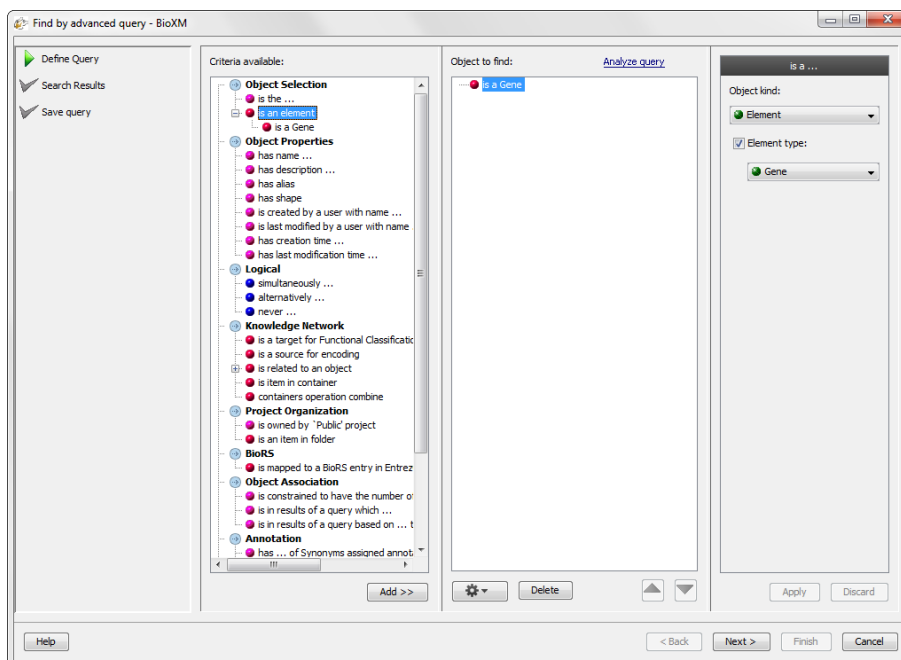


Figure 56. Creating a query — "Find by advanced query" wizard

3. In the "Criteria available" panel under "Knowledge Network" open "is related to an object" and select "is classified by a GO entry". Click the **"Add>>"** button to list it in the "Object to find" panel.
4. In the "Criteria available" panel under "Object properties" select "has name...". Click the **"Add>>"** button to list it in the "Object to find" panel. Enter "signal transduction" in the "Pattern" field in the right panel and click the **"Apply"** button.

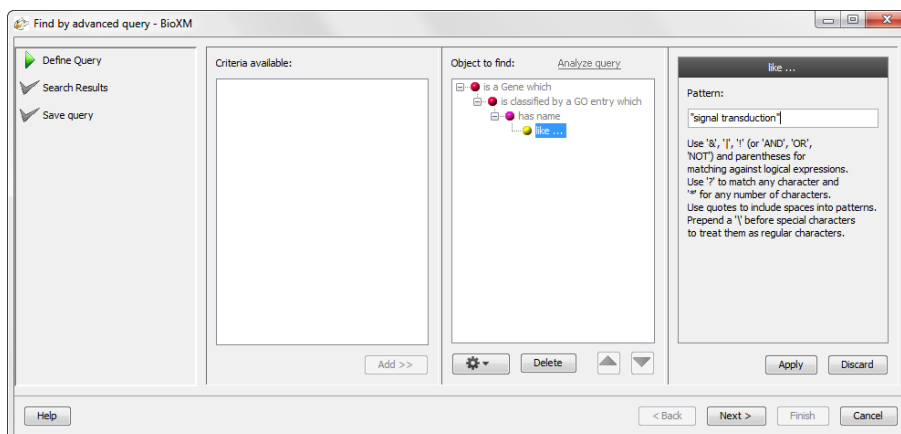


Figure 57. Creating a query — defining criteria

A natural language description of the query is "Find all objects which are genes which are classified by a GO entry like 'signal transduction'."

3.4. Displaying the query results

1. Click the **"Next>"** button to display the query results.

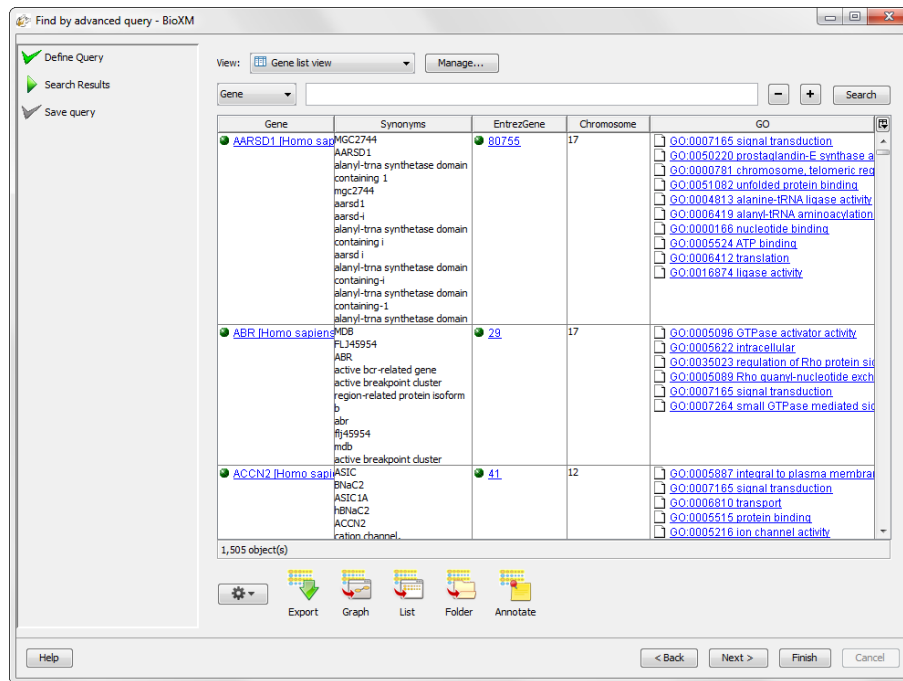


Figure 58. Creating a query — displaying query results

- The results include 1505 objects: genes which are assigned the "GO:0007165 signal transduction" entry; however, we actually want a list of all genes involved in signal transduction. We will look at the results more closely to see if we have achieved this goal.
- One way to check the results is to open an entry in the "GO" column (e.g., click "GO:0007165 signal transduction") to display the detailed report. Click the "Derived Concepts" tab to display all concepts derived from the GO entry.
- To see other entries that may be involved in signal transduction, select the "Description" column, enter the term "signal transduction" and click the **Search** button.

GO entries with a description including the term "signal transduction" are displayed (e.g., "GO:0000076 DNA replication checkpoint" or "GO:0000750 pheromone-dependent signal transduction involved in conjugation with cellular fusion"). We need to refine our search to include such entries.

- Close the "GO:0007165 signal transduction" window to return to the query wizard.

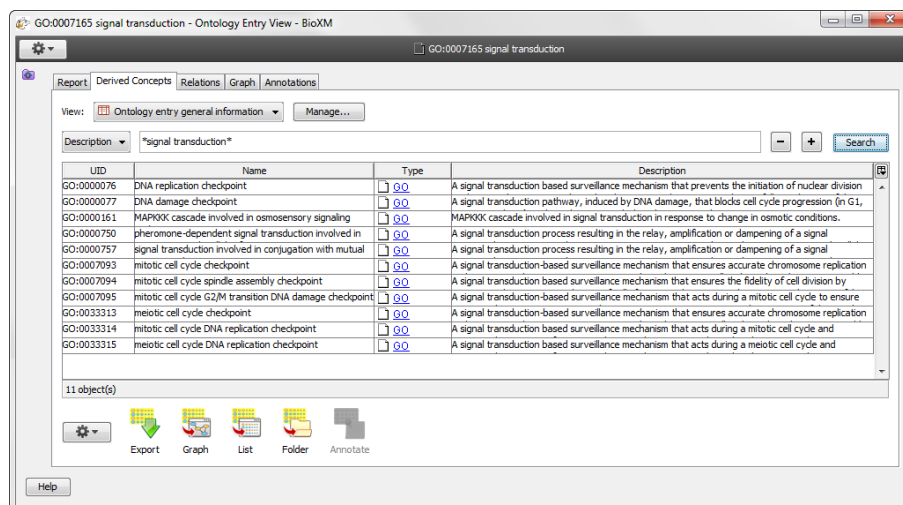


Figure 59. Creating a query — checking the results

3.5. Redefining the query

We will redefine the query to include all entries which are assigned the "GO:0007165 signal transduction" classification or are inferred from such entries.

1. Click the **"Back"** button to redefine the query.
2. In the "Object to find" panel click the "has name" criteria to select it and click the **"Delete"** button. Click "Yes" in the dialog to confirm the deletion.
3. In the "Criteria available" panel under "Knowledge Network" select "is inferred by ontology entry which..." and click the **"Add>>"** button to list it in the "Object to find" panel.
4. In the "Criteria available" panel under "Object properties" select "has name..." and click the **"Add>>"** button to list it in the "Object to find" panel. Enter "signal transduction" in the "Pattern" field in the right panel and click the **"Apply"** button.

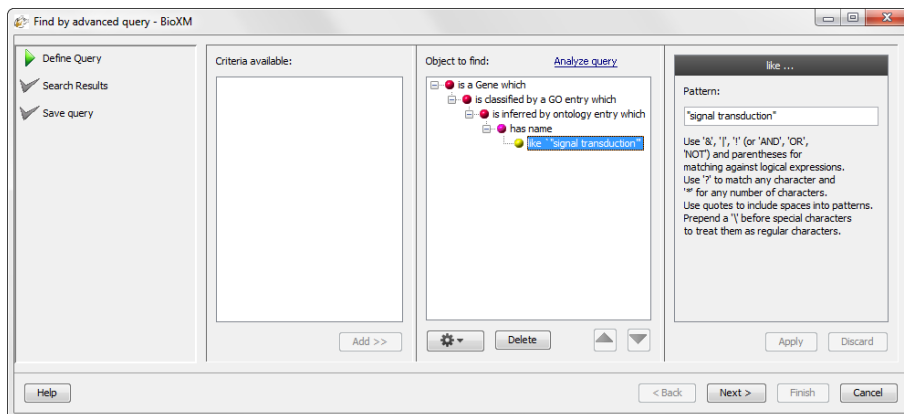


Figure 60. Creating a query — redefining criteria

A natural language description of the query is "Find all objects which are genes which are classified by a GO entry that is inferred by an entry like 'signal transduction'."

5. Click the **"Next>"** button to display the query results.

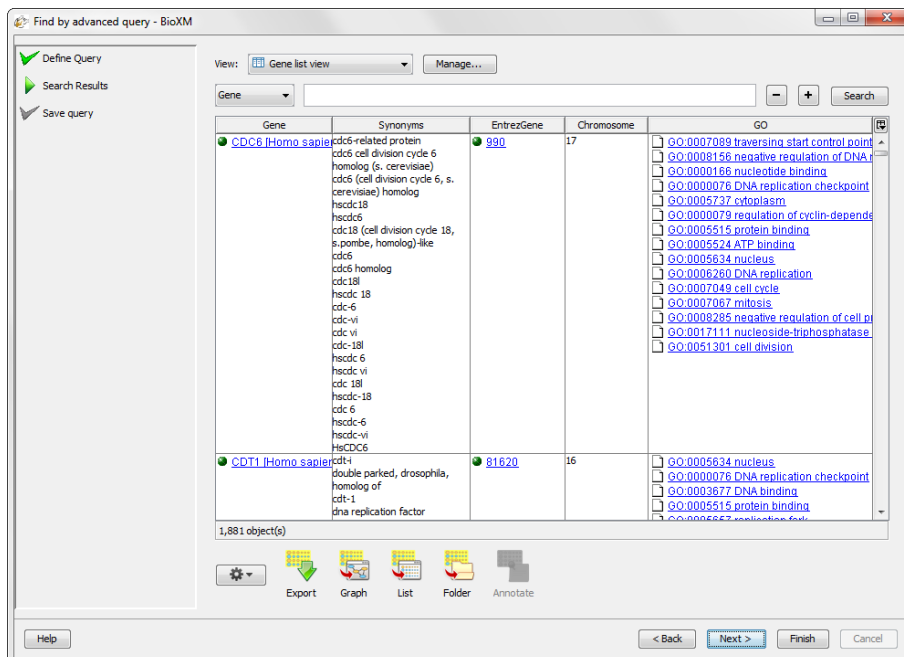


Figure 61. Creating a query — displaying refined query results

- The results include all genes which are assigned the "GO:0007165 signal transduction" entry and all genes which are assigned entries derived from the signal transduction entry (1881 objects in total).

3.6. Saving the query and creating a smart folder

- Click the "**Next>**" button in the "Search results" window to save the query and create a smart folder. The "Save query" window will be displayed.

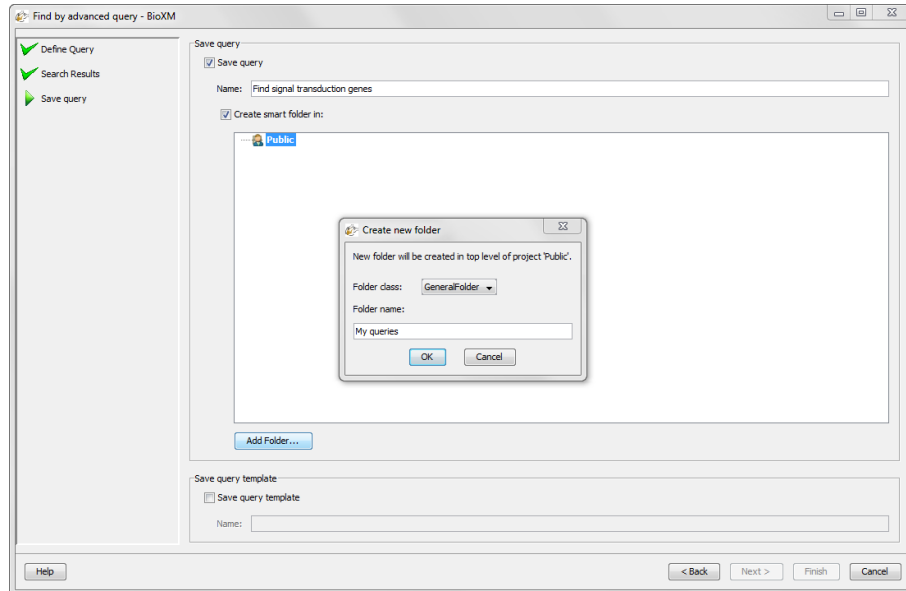


Figure 62. Saving the a query and creating a smart folder

- Click the "Save query" check box and enter a name (e.g., "Find signal transduction genes") for the query.
- Click the "Create smart folder in" check box. Select the "Public" folder and click the "**Add Folder...**" button.
- Enter a name for the folder ("My queries") and click "**OK**" to close the dialog.
- Click the "**Finish**" button to close the query wizard.

The "My queries" folder containing the "Find signal transduction genes" smart folder will be created in the "Public" project and is accessible using the project tree (see Figure 63: "Selecting a smart folder in the project tree").

3.7. Editing the smart folder

Next, we will make a more general query that can handle variables. This will allow us to perform more flexible queries to find genes by function in general, i.e., genes related to any GO terms, not only "signal transduction". The general query is similar to the "Find signal transduction genes" query, so we can simply duplicate that query and edit it.

- In the project tree, select the "Find signal transduction genes" smart folder. Right click the smart folder and select "Duplicate folder".

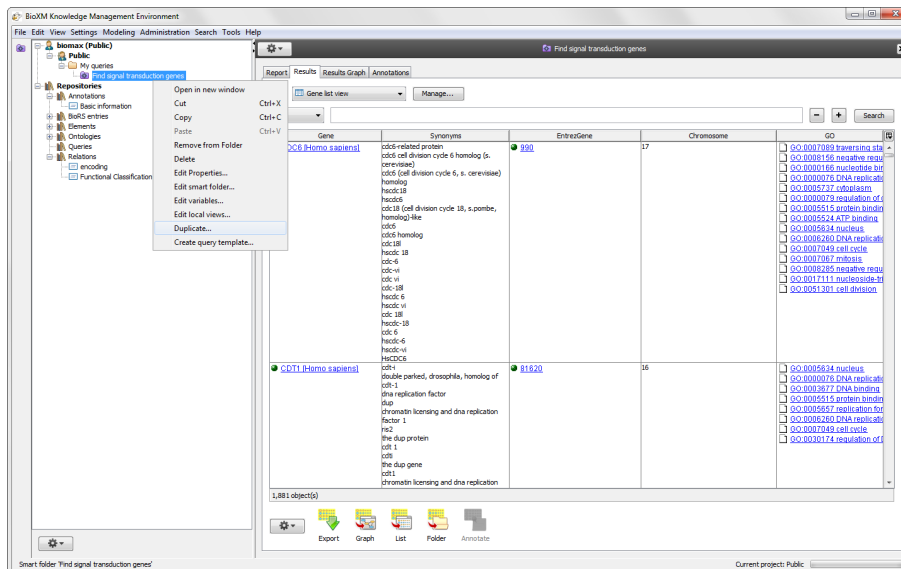


Figure 63. Selecting a smart folder in the project tree

Enter "Find genes by function" to rename the smart folder.

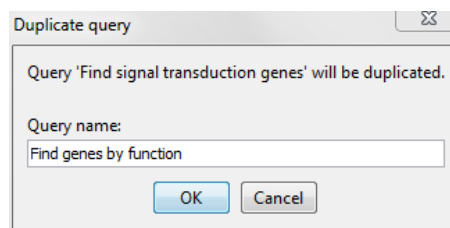


Figure 64. Duplicating a smart folder

2. In the project tree, select the "Find genes by function" smart folder. Right click the smart folder and select "Edit smart folder..." to display the "Edit query" dialog.

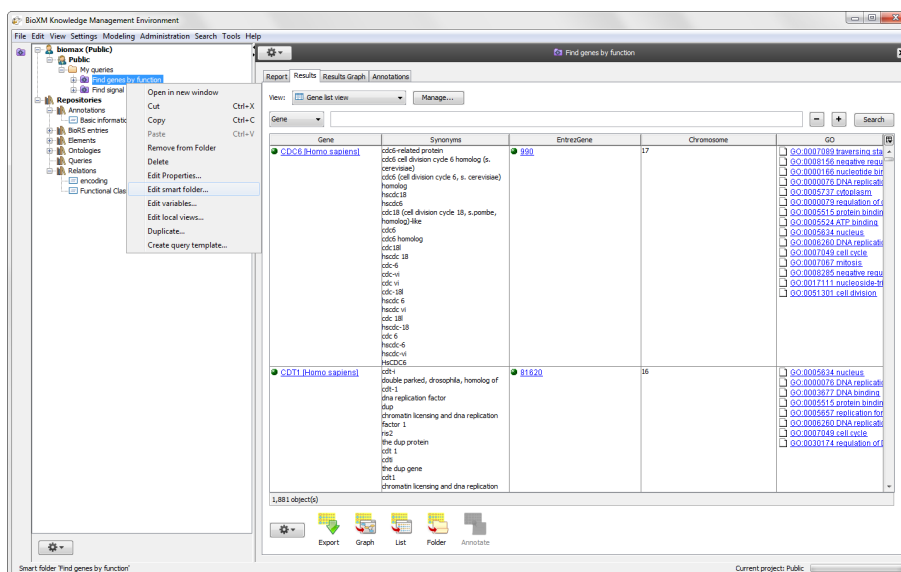


Figure 65. Selecting a smart folder to edit in the project tree

- We will edit the query to create a more general query to find genes by functions specified by a GO term. In the "Object to find" panel, select the criteria "like signal transduction" to display the "like..." panel on the right. In the right panel, check the "Use variables" check box and click the **"Introduce variable"** button.

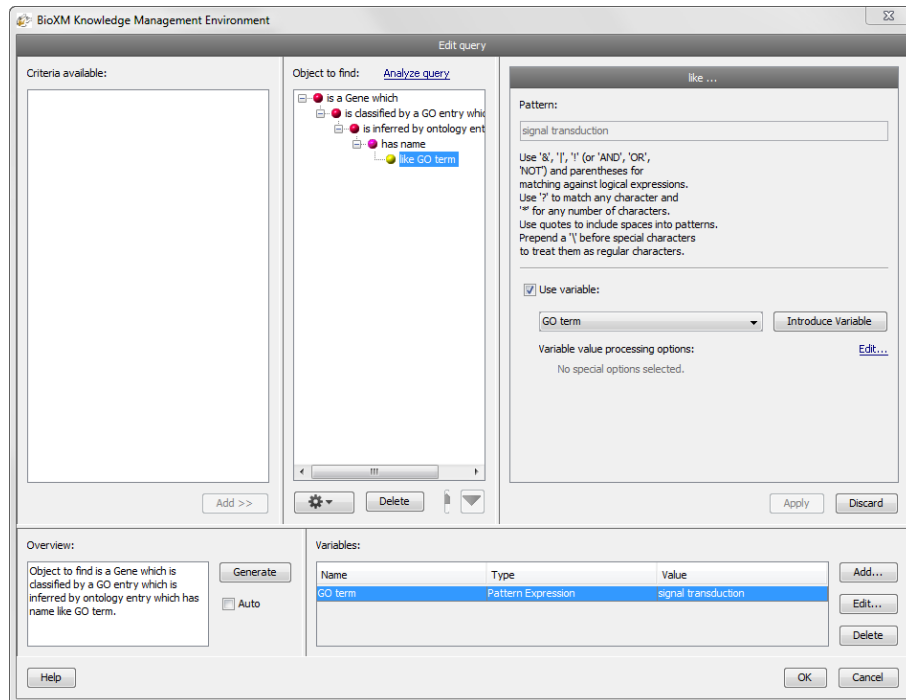


Figure 66. Editing a smart folder query

- In the "Variables" field, click the entry "Name" and click the **"Edit"** button to display the "Edit variable" dialog.

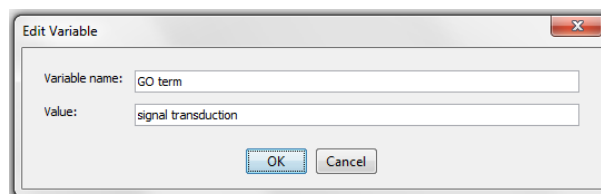


Figure 67. Adding variables to a query

Enter "GO term" as the variable name and any text in the "Value" field. We will enter "signal transduction" to set it as the default variable value for the query. Click the **"OK"** button to define the variable and close the dialog.

- In the right panel of the "Edit query" window, select "GO term" from the drop-down menu and click the **"Apply"** button.
- In the "Description" field, we can enter a description for the query or click the **"Generate"** button to generate a description from the query criteria. A natural language description of the query is "Find all genes which are classified by a GO entry which is inferred by an entry which has a name like 'any GO term'."
- Click the **"OK"** button to close the "Edit query" window and display the "Find genes by function" results tab.
- Click the **"Show Query Variables"** button to display the "GO term" variable field. Use "signal transduction" or enter another GO term in the field and click the **"Apply"** button. The query results will be displayed in the table.

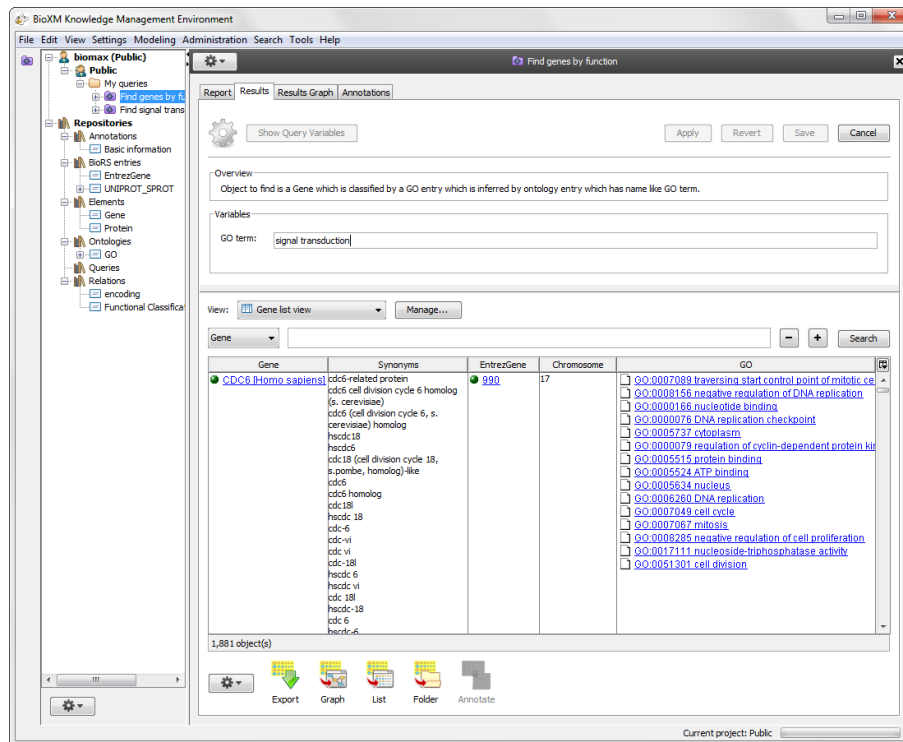


Figure 68. Using a variable query

The query results can be saved by clicking the **"Save"** button. See Section 3.6: "Saving the query and creating a smart folder".

4. Preparing a BioXM web portal

The first three sections have covered the basic steps to get started with the BioXM client software, create a data model, populate the knowledge base and perform typical queries. We will now set up a BioXM web portal to allow us to execute our query using a familiar Web interface rather than the BioXM client software. Instead of using the BioXM query builder and displaying a query in the BioXM interface, we can click a hyperlink to run the query and display the query results as a formatted table in a Web browser.

The BioXM Web Portal Builder has several functions for designing a BioXM Web interface for a specific project (e.g., customizing reports and query forms, making reports editable, defining dynamic thesauri, and setting up specific workflows and wizards), but we will focus on using the portal to run our queries and display the results.



Tip

We will cover the basic steps for using the BioXM web portal here. More information about the BioXM Web Portal Builder can be found on the BioXM Support Web. <https://ssl.biomax.de/info/biomax/bin/view/BioXM/PortalBuilder>. A working knowledge of HyperText Markup Language (HTML) and Foswiki is helpful. <http://foswiki.org/System/WebHome> provides numerous Foswiki materials.

4.1. Logging into a BioXM web portal

To login into a BioXM web portal complete the following steps:

1. Open a browser and enter the URL for the BioXM web portal login window. The login page will be displayed.
2. Enter you user name and password. Click the **"Login"** button. The BioXM web portal entry page will be displayed.

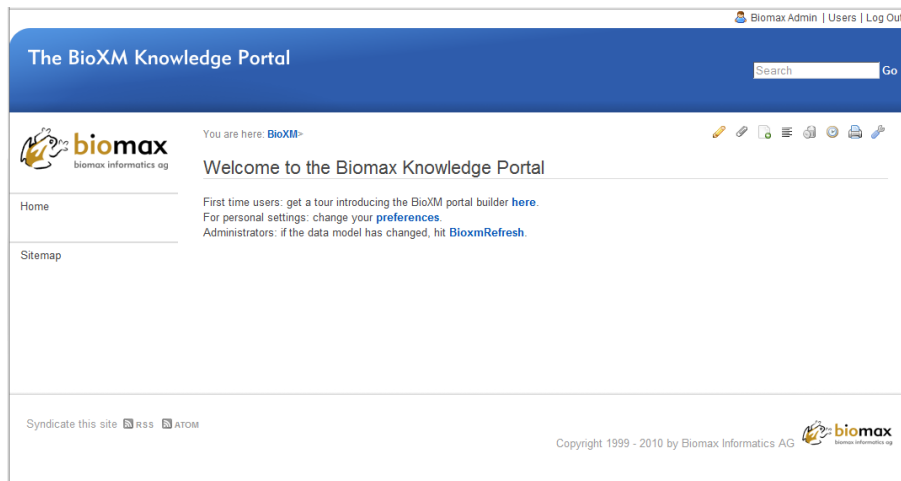


Figure 69. Opening the BioXM web portal

The content and design of this page will vary depending on your installation, but the functionality will be similar to what is described here.



Tip

Administrators may need to click the "BioxmRefresh" link if the data model has had significant changes.

4.2. Setting up a query in the BioXM web portal

The BioXM web portal can be used to execute only queries that already exist in the BioXM system. The principle approach is to first create queries using the BioXM query builder, which we have done already, create a wiki page for the query and then implement calls of the appropriate web portal plugins into the page. To create a wiki page and implement the plugins complete the following steps:

1. Click the "Edit" tool  (in the toolbar near the top right corner) to display the Foswiki editing interface.

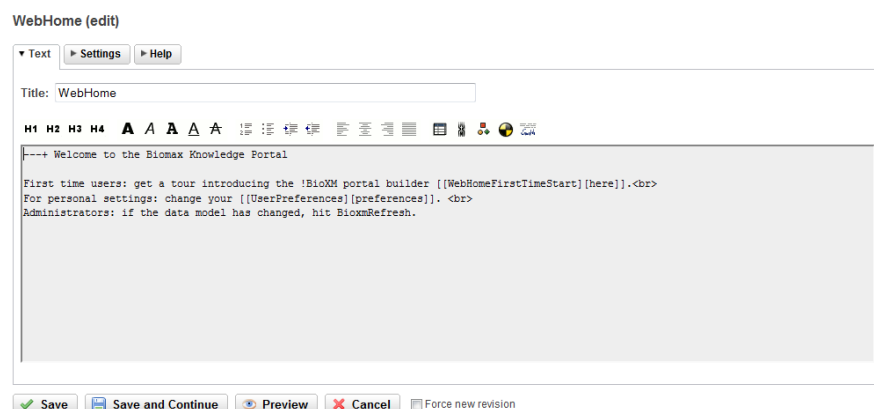


Figure 70. Foswiki editing interface

Here we can change the content of the "WebHome" page, the BioXM web portal entry page using Foswiki markup.

2. First we will create a page to run the "Find signal transduction genes" query and display the results.

New pages in the Foswiki system are called "topics" and are named using a "WikiWord". A WikiWord is a string containing at least two uppercase letters, one of which is the first letter of the word (e.g., NewPage). Any such string can be used, but we will use the names of our queries as in the BioXM client for simplicity.

Enter the following text to create a heading "Queries of interest" (indicated by the "----+") and a page for the query called "FindSignalTransductionGenes".

```
----+ Queries of interest

* FindSignalTransductionGenes
```

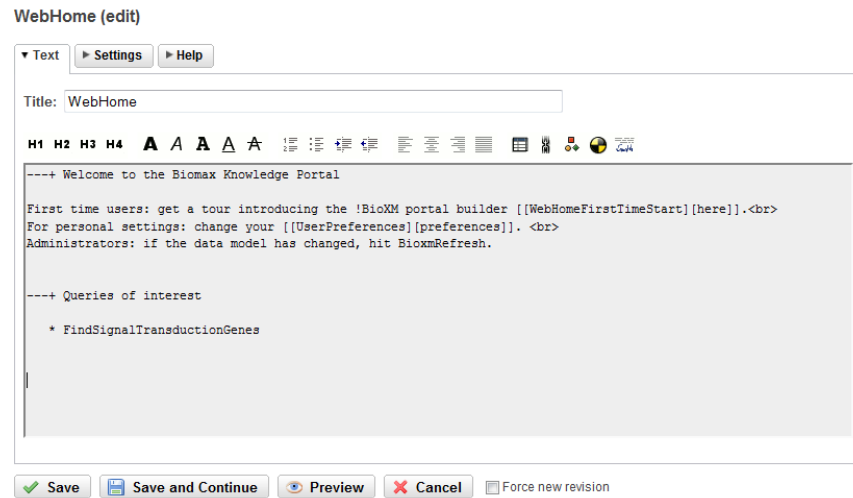


Figure 71. Editing the "WebHome" page

- Click the **"Save"** button. The edited "WebHome" page will be displayed.

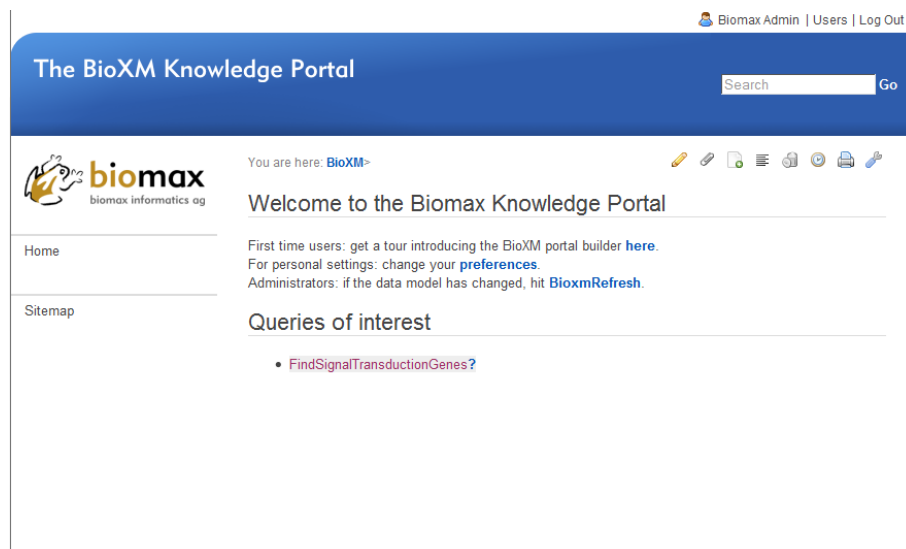


Figure 72. Displaying a new topic in the "WebHome" page

- Click the question mark (?) next to the "FindSignalTransductionGenes" text to edit the new page. The Foswiki editing interface for the new page, which is similar to the "WebHome" editing interface, will be displayed.
- We will edit the page to include a heading called "Find signal transduction genes" and a BioXM plugin to list the content of the smart folder of that name. Listing the contents of smart folders (i.e., executing BioXM queries) is done using the following general plugin call:

```
%BIOXM_QUERY{ query="query_name" } %
```


To add the "Find signal transduction genes" query, enter the following text.

```
%BIOXM_QUERY{query="Find signal transduction genes"}%
```

Figure 73. Adding the query plugin

The BioXM Knowledge Portal

You are here: [BioXM](#) > [Find SignalTransductionGenes](#)

Find signal transduction genes

1881 items found

Home Gene [] Search Rows 25 Page 1 of 76 Prev Next

Gene	Synonyms	EntrezGene	Chromosome	GO
cdc6 (Homo sapiens) cdc6-related protein cdc6 (cell division cycle 6 homolog (s. cerevisiae)) cdc6 (cell division cycle 6, s. cerevisiae) homolog hscdc18 hscdc5 cdc18 (cell division cycle 18, s. pombe, homolog)-like cdc5 cdc6 homolog cdc18l hscdc18 hscdc6 cdc-vl cdc-18l hscdc5 hscdc-vl cdc-18l hscdc5 cdc-18l hscdc18 cdc-6 hscdc-9 hscdc-vl HSCDC5 CDC-18L HSCDC18 CDC5	950 17	<input type="checkbox"/> GO:0007089 traversing start control point of mitotic cell cycle <input type="checkbox"/> GO:0000156 negative regulation of DNA replication <input type="checkbox"/> GO:0000166 nucleotide binding <input type="checkbox"/> GO:0000076 DNA replication checkpoint <input type="checkbox"/> GO:0005737 cytoskeleton <input type="checkbox"/> GO:0000079 regulation of cyclin-dependent protein kinase activity <input type="checkbox"/> GO:0005515 protein binding <input type="checkbox"/> GO:0005524 ATP binding <input type="checkbox"/> GO:0005634 nucleus <input type="checkbox"/> GO:0006260 DNA replication <input type="checkbox"/> GO:0007049 cell cycle <input type="checkbox"/> GO:0007067 mitosis <input type="checkbox"/> GO:0008285 negative regulation of cell proliferation <input type="checkbox"/> GO:0017111 nucleoside-triphosphatase activity <input type="checkbox"/> GO:0051301 cell division		
COT1 (Homo sapiens) cot1 double parted, drosophila, homolog of cot-1 dna replication factor dup chromatin licensing and dna replication factor 1 ml2 the dup protein cot1 cot the dup gene cot1	81620 16	<input type="checkbox"/> GO:0005634 nucleus <input type="checkbox"/> GO:0000076 DNA replication checkpoint <input type="checkbox"/> GO:0003677 DNA binding <input type="checkbox"/> GO:0005515 protein binding <input type="checkbox"/> GO:0005657 replication fork <input type="checkbox"/> GO:0006260 DNA replication <input type="checkbox"/> GO:0007049 cell cycle <input type="checkbox"/> GO:0030174 regulation of DNA-dependent DNA replication initiation		

The same steps can be used to add the second query "Find genes by function".

- 46

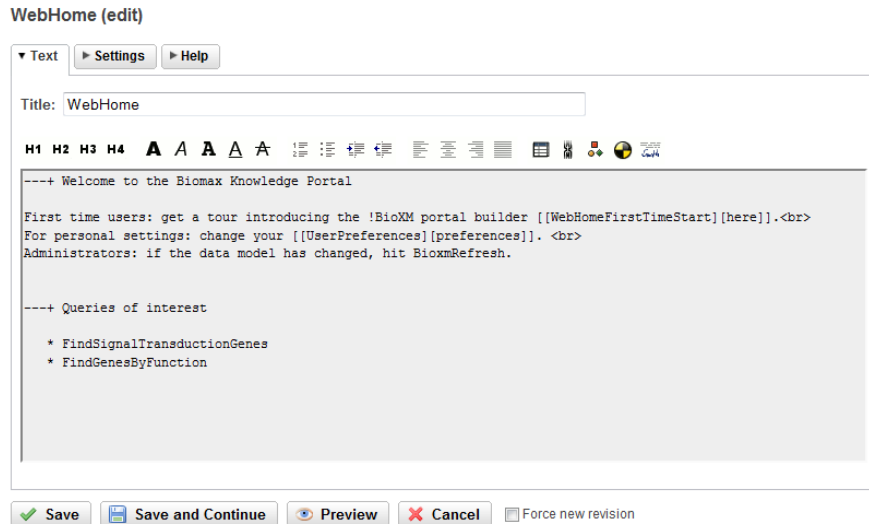


Figure 75. Editing the "WebHome" page

2. Open the new page by clicking "FindGenesByFunction" in the "WebHome page".

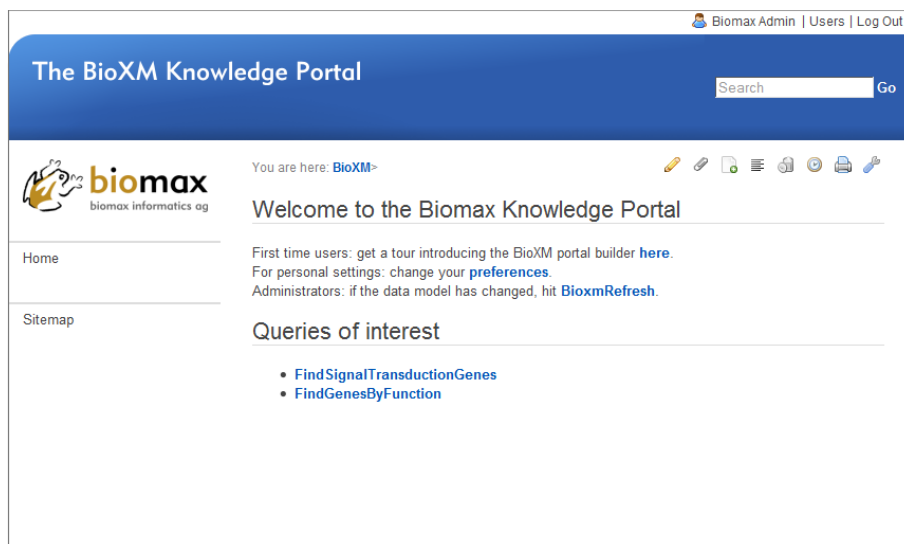



Figure 76. Displaying the "WebHome" page

3. Edit the page by clicking the "Edit" tool  to display the Foswiki editing interface. We will edit the page to include the plugin for the query.

Executing a BioXM query that uses variables is done using the following general plugin call:

```
%BIOXM_QUERY{query="query_name" variables="var1=value;var2=value"}%
```

The `variables` parameter fixes the query variable values. Omitting this parameter will lead to a query form in which values can be entered by the user; this is what we want to do. To edit the page to include the plugin for the query without fixing the variable values, enter the following text and click "Save".

```
---+ Find genes by function

%BIOXM_QUERY{query="Find genes by function"}%
```

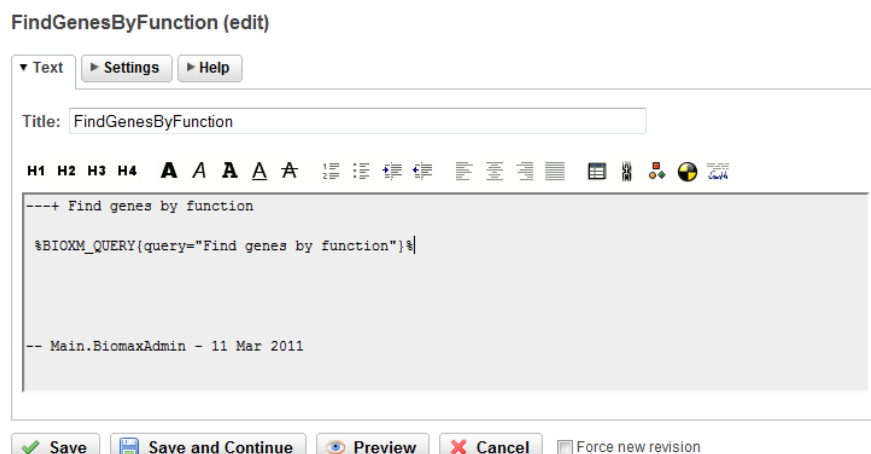


Figure 77. Editing the "FindGenesByFunction" page

The "FindGenesByFunction" page will be displayed with a field for entering any GO term.

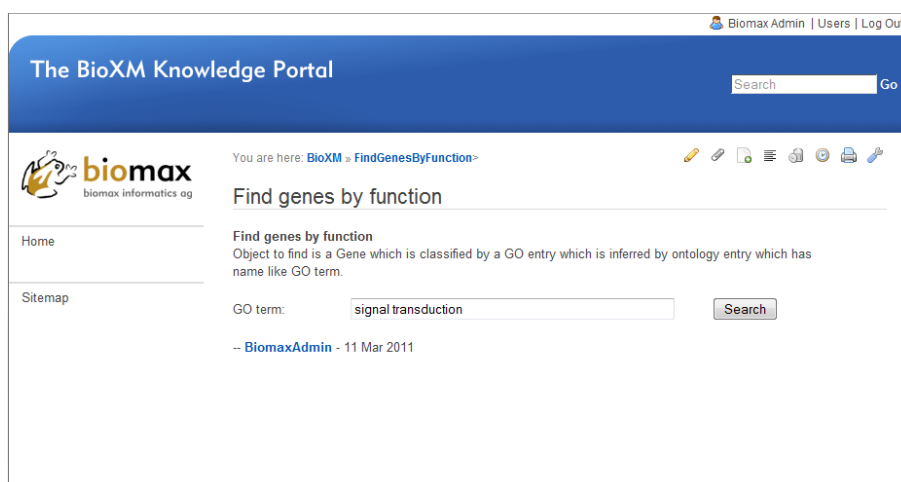


Figure 78. Displaying the "FindGenesByFunction" page

4. Use the default term "signal transduction" or enter any other GO term and click the "Search" button. The query results will be displayed.

4.3. Displaying an object report in the web portal

Information about each gene can be displayed in an object report by clicking the hyperlink in the "Gene" column. Like any other view, object reports can be tailored to display particular information. Next we will display an object report and use a predefined view tailored for use in the BioXM web portal. We will modify the view to allow the object report to be annotated directly in the web portal

- 49

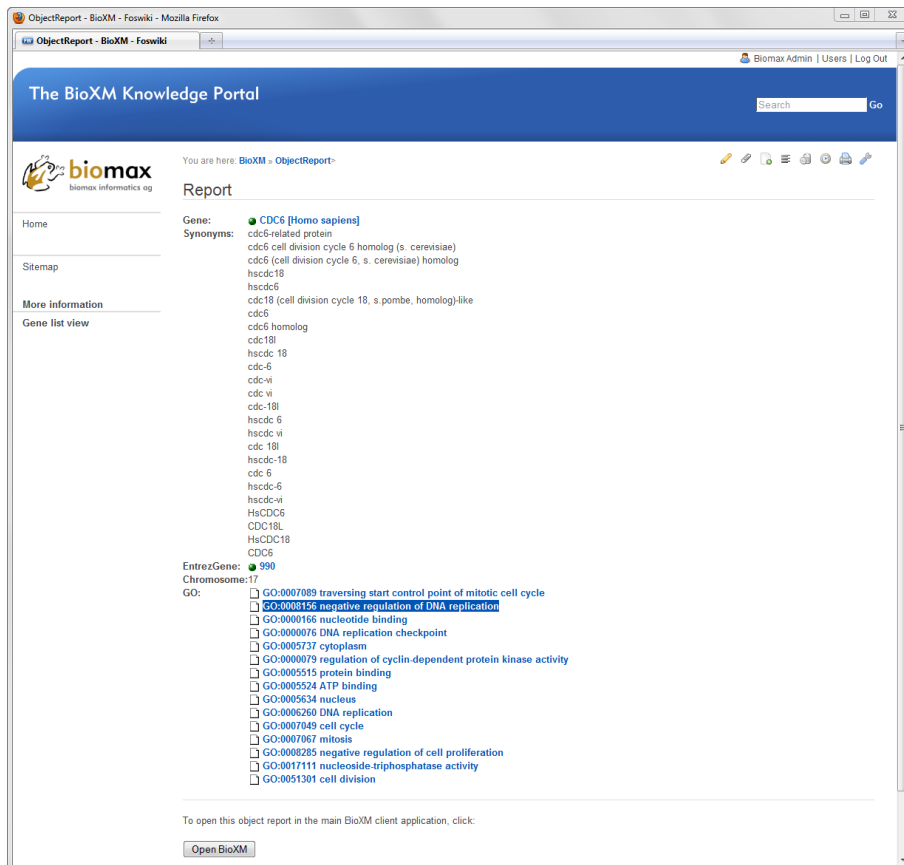


Figure 80. Displaying the object report for a gene

The current object report for genes simply lists the information defined for the gene list view; however, we can use a predefined view to display an object report layout designed specifically for the web portal. To do this, we will first define a new object report view using the BioXM client software.

2. Open the BioXM client software and select "*Administration* → *Views...*" to display the "Views" dialog.

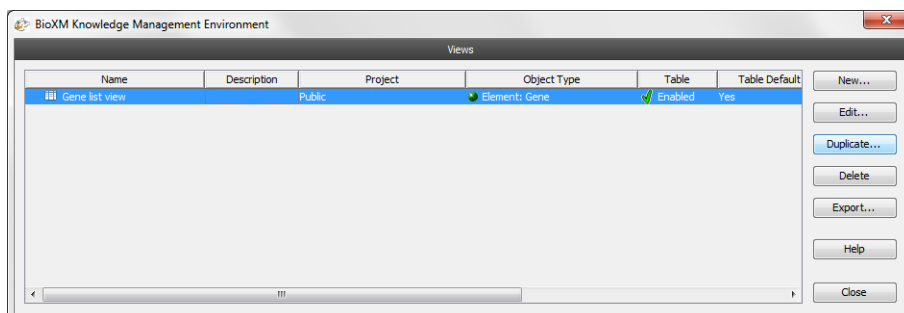


Figure 81. Displaying the "Views" dialog in the BioXM client

3. Select the "Gene list view" and click the "Duplicate..." button. The "Duplicate view" dialog will be displayed.

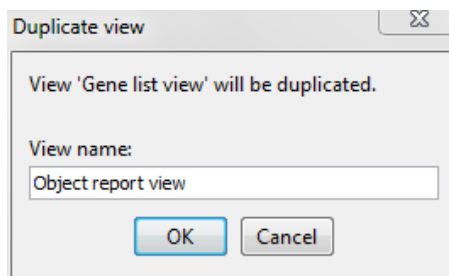


Figure 82. Displaying the object report for a gene

4. Enter a new name (e.g., "Object report view") for the view in the dialog field. Click the **"OK"** button. The "Views" dialog will be displayed again.
5. Select the "Object report view" and click the **"Edit"** button to display the "Edit view" window.

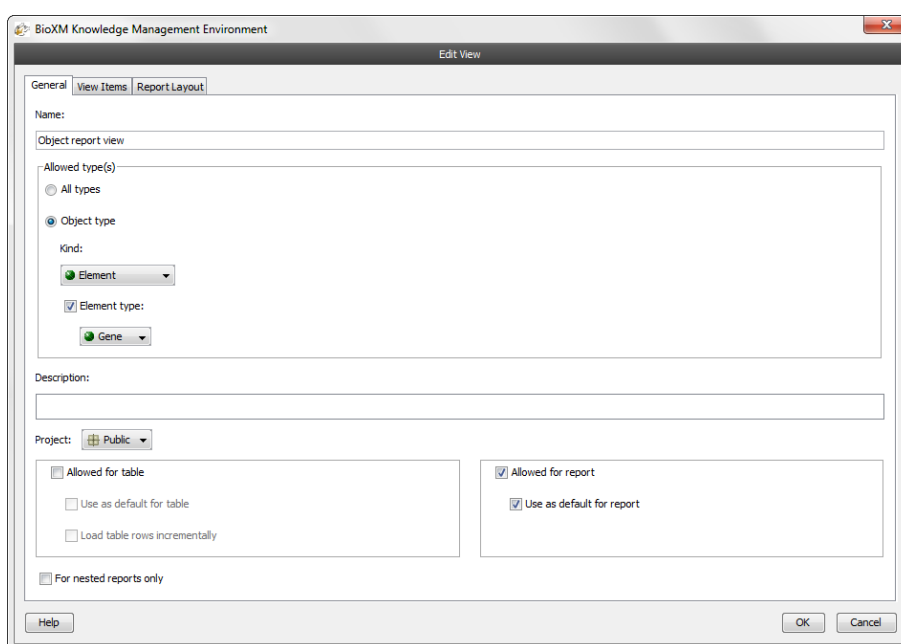


Figure 83. Defining the object report view

6. In the "General" tab remove the check from the "Allowed for table" check box so the view applies to single objects only, not to tables of objects.
7. Click the "View items" tab to open it.

Instead of only showing the "Synonyms" assigned annotation attribute, we will display the assigned annotation form. This allows the annotation to be edited in both the BioXM client software and the BioXM web portal.

8. In middle panel, under "View items" select "Synonyms" and click the **"Delete"** button. Click "Yes" to confirm the deletion.
9. In the "Available view items" panel on the left, under "Annotation" select "Assigned annotation" and click the **"Add>>"** button. In the right panel, select the "Annotation form" check box and select "Basic information" from the drop-down menu. Click the **"Apply"** button.

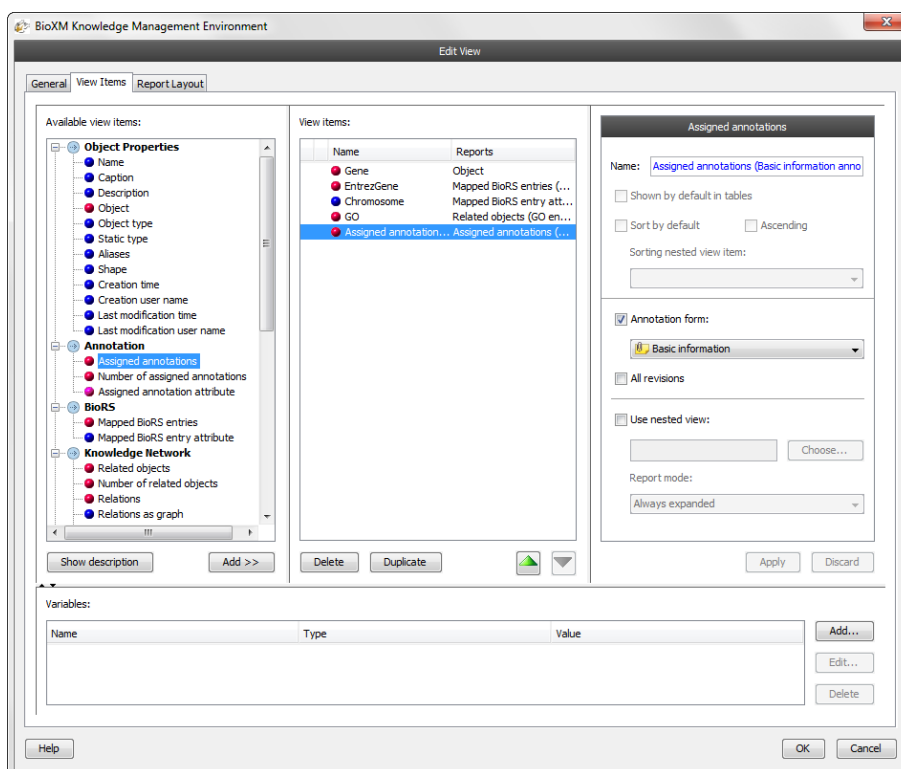


Figure 84. Adding assigned annotation in the object report view

- Click the "Report Layout" tab to open it. Select the "Predefined" radio button and select "Portal view" from the drop-down menu.

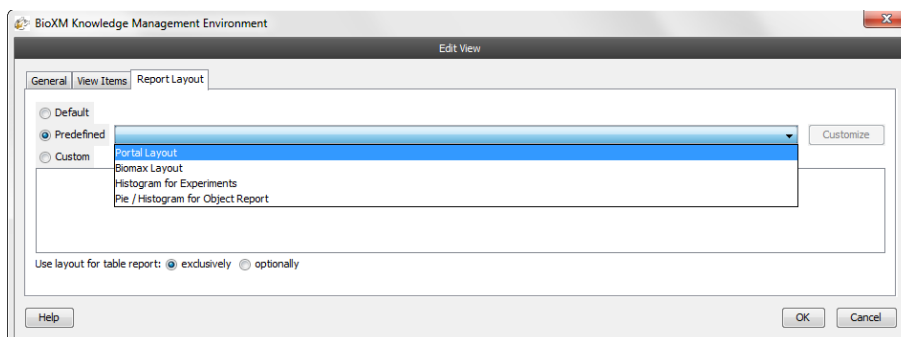


Figure 85. Selecting the predefined layout for the object report view

- Click the "OK" button to close the "Edit view" window. Click "Close" to close the "Views" window.
- We can now return to the BioXM web portal. Reload the gene object report to show the new object report layout.

The BioXM Knowledge Portal

You are here: BioXM » ObjectReport

Search Go

Report

CDC6 [Homo sapiens]

Gene	CDC6 [Homo sapiens]
EntrezGene	990
Chromosome	17
GO	<ul style="list-style-type: none"> GO:0007089 traversing start control point of mitotic cell cycle GO:0008156 negative regulation of DNA replication GO:0000166 nucleotide binding GO:0000076 DNA replication checkpoint GO:0005737 cytoplasm GO:0000079 regulation of cyclin-dependent protein kinase activity GO:0005515 protein binding GO:0005524 ATP binding GO:0005634 nucleus GO:0006260 DNA replication GO:0007049 cell cycle GO:0007067 mitosis GO:0008285 negative regulation of cell proliferation GO:0017111 nucleoside-triphosphatase activity GO:0051301 cell division

Assigned annotations (Basic information annotations)

Synonyms	<p>cdc6-related protein</p> <p>cdc6 cell division cycle 6 homolog (s. cerevisiae)</p> <p>cdc6 (cell division cycle 6, s. cerevisiae) homolog</p> <p>hscdc18</p> <p>hscdc6</p> <p>cdc18 (cell division cycle 18, s. pombe, homolog)-like</p> <p>cdc6</p> <p>cdc6 homolog</p> <p>cdc18l</p> <p>hscdc 18</p> <p>cdc-6</p> <p>cdc-vi</p> <p>cdc-vi</p> <p>cdc-18l</p> <p>hscdc 6</p> <p>hscdc-vi</p> <p>cdc 18l</p> <p>hscdc-18</p> <p>cdc 6</p> <p>hscdc-6</p> <p>hscdc-vi</p> <p>HsCDC6</p> <p>CDC18L</p> <p>HsCDC18</p> <p>CDC6</p>
----------	------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

[Edit](#)

To open this object report in the main BioXM client application, click:

[Open BioXM](#)

Syndicate this site [RSS](#) [ATOM](#)

Copyright 1999 - 2010 by Biomax Informatics AG

Figure 86. Displaying the predefined object report for a gene

13. The "Assigned annotations" table can be edited. Click the **"Edit"** button below the table to edit the annotation. Click the **"Submit"** button to commit the changes.

Assigned annotations (Basic information annotations)

Assigned annotations (Basic information annotations)	
Synonyms	cdc6-related protein
	cdc6 cell division cycle 6 homolog (s. cerevisiae)
	cdc6 (cell division cycle 6, s. cerevisiae) homolog
	hscdc18
	hscdc6
	cdc18 (cell division cycle 18, s.pombe, homolog)-like
	cdc6
	cdc6 homolog
	cdc18l
	hscdc 18
	cdc-6
	cdc-vi
	cdc vi
	cdc-18l
	hscdc 6
	hscdc vi
	cdc 18l
	hscdc-18
	cdc 6
	hscdc-6
	hscdc-vi
	HsCDC6
	CDC18L
	HsCDC18
	CDC6

Submit Cancel

Figure 87. Editing the assigned annotation for a gene

This concludes the steps for getting started with the BioXM web portal.

5. Getting help

For more information about using the BioXM Knowledge Management Environment see the *BioXM User Manual* or the BioXM online help. To open the BioXM online help, select "*Help → Online Help...*" from the BioXM main menu. The BioXM online help will open in a new window.

6. Logging out

6.1. Logging out of the BioXM client application

You can log out of the BioXM client application by selecting one of the following options from the main menu:

- "*File → Log Out...*" — log out the current user without exiting the BioXM application; you can subsequently log in again with the same or different user name
- "*File → Exit BioXM...*" — log out the current user and exit the BioXM application

Additionally, you can log out and exit the BioXM application by closing the main application window. A confirmation dialog will be displayed before you are logged out and the application closes.

6.2. Logging out of the BioXM web portal

You can log out of the BioXM web portal by clicking the "Log Out" link in the top right corner.